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(54) Title: GROWTH DIFFERENTIATION FACTOR-8 (57) Abstract A transgenic non-human animal of the species selected from the group consisting of avian, bovine, ovine and porcine having a transgene which results in disrupting the production of and/or activity of growth differentiation factor-8 (GDF-8) chromosomally integrated into the germ cells of the animal is disclosed. Also disclosed are methods for making such animals, and methods of treating animals, including humans, with antibodies or antisense directed to GDF-8. The animals so treated are characterized by increased muscle tissue.		

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AMENDED CLAIMS

[received by the International Bureau on 21 July 1998 (21.07.98);
original claim 2 amended; new claims 49-65 added;
remaining claims unchanged (4 pages)]

1. A transgenic non-human animal having a transgene disrupting or interfering with expression of growth differentiation factor-8 (GDF-8) chromosomally integrated into the germ cells of the animal.
2. The transgenic animal of claim 1, wherein the animal is selected from the group of species consisting of murine, avian, bovine, ovine, piscine, murine, and porcine.
3. The transgenic animal of claim 1 where the species is avian.
4. The transgenic animal of claim 1 where the species is bovine.
5. The transgenic animal of claim 1 where the species is porcine.
6. The transgenic animal of claim 1 where the species is ovine.
7. The transgenic animal of claim 1 where the species is piscine.
8. The transgenic animal of claim 1, wherein the transgene comprises GDF-8 antisense polynucleotide(s).
9. The transgenic animal of claim 1, wherein the transgene comprises a gene encoding a dominant negative GDF-8 polypeptide.
10. The transgenic animal of claim 1, wherein the animal is homozygous or heterozygous for GDF-8 polynucleotide.
11. A chicken or turkey egg produced by the transgenic animal of claim 3.

44. A method for identifying a compound that affects GDF-8 activity or gene expression comprising:
- a) incubating the compound with GDF-8 polypeptide, or with a recombinant cell expressing GDF-8 under conditions sufficient to allow the components to interact; and
 - b) determining the effect of the compound on GDF-8 activity or expression.
45. The method of claim 44, wherein the effect is inhibition of GDF-8 activity or expression.
46. The method of claim 44, wherein the effect is stimulation of GDF-8 activity or expression.
47. An isolated polynucleotide encoding a truncated GDF-8 polypeptide wherein the truncation is a loss of the C-terminal active fragment of GDF-8.
48. The isolated polynucleotide of claim 47, wherein the polynucleotide is as shown in FIGURE 12a.
49. The transgenic animal of claim 1 where the species is murine.
50. A method for producing a transgenic non-human animal having a phenotype characterized by expression of a transgene otherwise not naturally occurring, wherein expression of the transgene disrupts or interferes with growth differentiation factor-8 (GDF-8) activity, comprising:
- a) introducing a transgene in operable linkage with at least one expression regulatory sequence into a zygote of an animal;
 - b) transplanting the zygote of a) into a pseudopregnant animal;
 - c) allowing the zygote to develop to term; and
 - d) identifying at least one transgenic offspring from c) where expression of the transgene disrupts or interferes with GDF-8 activity.

51. The method of claim 50, wherein the introduction of the transgene into the embryo is by introducing an embryonic stem cell containing the transgene into the embryo.
52. The method of claim 50, wherein the introduction of the transgene into the embryo is by infecting the embryo with a virus containing the transgene.
52. The method of claim 52, wherein the virus is a retrovirus.
53. The method of claim 50, wherein the transgene encodes GDF-8 antisense polynucleotide(s).
54. The method of claim 50, wherein the transgene encodes a dominant negative protein that disrupts or interferes with GDF-8 activity.
55. The method of claim 50, wherein the transgenic animal is homozygous or heterozygous for GDF-8 polynucleotide.
56. The method of claim 50, wherein disrupting or interfering with GDF-8 activity in the transgenic non-human animal produces increased muscle mass as compared to a non-transgenic animal of the same species.
57. The method of claim 50, wherein the animal is selected from the group consisting of murine, avian, bovine, ovine, piscine, and porcine.

58. A method for producing a transgenic non-human animal having a phenotype characterized by expression of a transgene otherwise not naturally occurring, wherein expression of the transgene disrupts or interferes with expression of growth differentiation factor-8 (GDF-8), comprising:
- a) introducing a transgene in operable linkage with at least one expression regulatory sequence into a zygote of an animal;
 - b) transplanting the zygote of a) into a pseudopregnant animal;
 - c) allowing the zygote to develop to term; and
 - d) identifying at least one transgenic offspring from c) where expression of the transgene disrupts or interferes with expression of GDF-8.
59. The method of claim 58, wherein the introduction of the transgene into the embryo is by introducing an embryonic stem cell containing the transgene into the embryo.
60. The method of claim 58, wherein the introduction of the transgene into the embryo is by infecting the embryo with a virus containing the transgene.
61. The method of claim 60, wherein the virus is a retrovirus.
62. The method of claim 58, wherein the transgene encodes GDF-8 antisense polynucleotide(s).
63. The method of claim 58, wherein the transgenic animal is homozygous or heterozygous for GDF-8 polynucleotide.
64. The method of claim 58, wherein disrupting or interfering with GDF-8 activity in the transgenic non-human animal produces increased muscle mass as compared to a non-transgenic animal of the same species.
65. The method of claim 58, wherein the animal is selected from the group consisting of murine, avian, bovine, ovine, piscine, and porcine.

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The invention also provides a method for a method for identifying a compound that affects GDF-8 activity or gene expression including incubating the compound with GDF-8 polypeptide, or with a recombinant cell expressing GDF-8 under conditions sufficient to allow the compounds to interact and determining the effect of the compound on GDF-
5 8 activity or expression.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1a is a Northern blot showing expression of GDF-8 mRNA in adult tissues. The probe was a partial murine GDF-8 clone.

FIGURE 1b is a Southern blot showing GDF-8 genomic sequences identified in mouse,
10 rat, human, monkey, rabbit, cow, pig, dog and chicken.

FIGURE 2 shows partial nucleotide and predicted amino acid sequences of murine GDF-8 (FIGURE 2a; SEQ ID NO:11 and 12, respectively), human GDF-8 (FIGURE 2b; SEQ ID NO: 13 and 14, respectively), rat GDF-8 (FIGURE 2c; SEQ ID NO: 24 and 25, respectively) and chicken GDF-8 (FIGURE 2d; SEQ ID NO: 22 and 23, respectively).
15 The putative dibasic processing sites in the murine sequence are boxed.

FIGURE 3a shows the alignment of the C-terminal sequences of GDF-8 with other members of the TGF- β superfamily. The conserved cysteine residues are boxed. Dashes denote gaps introduced in order to maximize alignment.

FIGURE 3b shows the alignment of the C-terminal sequences of GDF-8 from human,
20 murine, rat and chicken sequences.

FIGURE 4 shows amino acid homologies among different members of the TGF superfamily. Numbers represent percent amino acid identities between each pair calculated from the first conserved cysteine to the C-terminus. Boxes represent homologies among highly-related members within particular subgroups.

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FIGURE 5 shows the sequence of GDF-8. Nucleotide and amino acid sequences of murine (FIGURE 5a and 5b)(GenBank accession number U84005; SEQ ID NO:11 and 12, respectively) and human (FIGURE 5c and 5d; SEQ ID NO:13 and 14, respectively) GDF-8 cDNA clones are shown. Numbers indicate nucleotide position relative to the 5' end. Consensus N-linked glycosylation signals are shaded. The putative RXXR proteolytic cleavage sites are boxed.

FIGURE 6 shows a hydropathicity profile of GDF-8. Average hydrophobicity values for murine (FIGURE 6a) and human (FIGURE 6b) GDF-8 were calculated using the method of Kyte and Doolittle (*J. Mol. Biol.*, 157:105-132, 1982). Positive numbers indicate increasing hydrophobicity.

FIGURE 7 shows a comparison of murine and human GDF-8 amino acid sequences. The predicted murine sequence is shown in the top lines and the predicted human sequence is shown in the bottom lines. Numbers indicate amino acid position relative to the N-terminus. Identities between the two sequences are denoted by a vertical line.

FIGURE 8 shows the expression of GDF-8 in bacteria. BL21 (DE3) (pLysS) cells carrying a pRSET/GDF-8 expression plasmid were induced with isopropylthio- β -galactoside, and the GDF-8 fusion protein was purified by metal chelate chromatography. Lanes: total=total cell lysate; soluble=soluble protein fraction; insoluble=insoluble protein fraction (resuspended in 10 mM Tris pH 8.0, 50 mM sodium phosphate, 8 M urea, and 10 mM β -mercaptoethanol [buffer B]) loaded onto the column, pellet=insoluble protein fraction discarded before loading the column; flow-through=proteins not bound by the column; washes=washes carried out in buffer B at the indicated pH's. Positions of molecular weight standards are shown at the right. Arrow indicates the position of the GDF-8 fusion protein.

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FIGURE 9 shows the expression of GDF-8 in mammalian cells. Chinese hamster ovary cells were transfected with pMSXND/GDF-8 expression plasmids and selected in G418. Conditioned media from G418-resistant cells (prepared from cells transfected with constructs in which GDF-8 was cloned in either the antisense or sense orientation) were
5 concentrated, electrophoresed under reducing conditions, blotted, and probed with anti-GDF-8 antibodies and [¹²⁵I]iodoprotein A. Arrow indicates the position of the processed GDF-8 protein.

FIGURE 10 shows the expression of GDF-8 mRNA. Poly A-selected RNA (5μg each) prepared from adult tissues (FIGURE 10a) or placentas and embryos (FIGURE 10b) at
10 the indicated days of gestation was electrophoresed on formaldehyde gels, blotted, and probed with full length murine GDF-8.

FIGURE 11 shows chromosomal mapping of human GDF-8. DNA samples prepared from human/rodent somatic cell hybrid lines were subjected to PCR, electrophoresed on agarose gels, blotted, and probed. The human chromosome contained in each of the
15 hybrid cell lines is identified at the top of each of the first 24 lanes (1-22, X, and Y). In the lanes designated M, CHO, and H, the starting DNA template was total genomic DNA from mouse, hamster, and human sources, respectively. In the lane marked B1, no template DNA was used. Numbers at left indicate the mobilities of DNA standards.

Figure 12a shows a map of the GDF-8 locus (top line) and targeting construct (second
20 line). The black and stippled boxes represent coding sequences for the pro- and C-terminal regions, respectively. The white boxes represent 5' and 3' untranslated sequences. A probe derived from the region downstream of the 3' homology fragment and upstream of the most distal HindIII site shown hybridizes to an 11.2 kb HindIII fragment in the GDF-8 gene and a 10.4 kb fragment in an homologously targeted gene.
25 Abbreviations: H, HindIII; X, Xba I.

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Figure 12b shows a Southern blot analysis of offspring derived from a mating of heterozygous mutant mice. The lanes are as follows: DNA prepared from wild type 129 SV/J mice (lane 1), targeted embryonic stem cells (lane 2), F1 heterozygous mice (lanes 3 and 4), and offspring derived from a mating of these mice (lanes 5-13).

- 5 Figure 13 shows the muscle fiber size distribution in mutant and wild type littermates. Figure 13a shows the smallest cross-sectional fiber widths measured for wild type (n = 1761) and mutant (n = 1052) tibialis cranial. Figure 13b shows wild type (n = 900) and mutant (n = 900) gastrocnemius muscles, and fiber sizes were plotted as a percent of total fiber number. Standard deviations were 9 and 10 μm , respectively, for wild type and
- 10 mutant tibialis cranial is and 11 and 9 μm , respectively, for wild type and mutant gastrocnemius muscles. Legend: o-o, wild type; _ _ , mutant.

Figure 14a shows the nucleotide and deduced amino acid sequence for baboon GDF-8 (SEQ ID NO:18 and 19, respectively).

- Figure 14b shows the nucleotide and deduced amino acid sequence for bovine GDF-8
- 15 (SEQ ID NO: 20 and 21, respectively).

Figure 14c shows the nucleotide and deduced amino acid sequence for chicken GDF-8 (SEQ ID NO:22 and 23, respectively).

Figure 14d shows the nucleotide and deduced amino acid sequence for rat GDF-8 (SEQ ID NO:24 and 25, respectively).

- 20 Figure 14e shows the nucleotide and deduced amino acid sequence for turkey GDF-8 (SEQ ID NO:26 and 27, respectively).

Figure 14f shows the nucleotide and deduced amino acid sequence for porcine GDF-8 (SEQ ID NO:28 and 29, respectively).

- Figure 14g shows the nucleotide and deduced amino acid sequence for ovine GDF-8
- 25 (SEQ ID NO:30 and 31, respectively).

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Figures 15a and 15b show an alignment between murine, rat, human, porcine, ovine, baboon, bovine, chicken, and turkey GDF-8 amino acid sequences (SEQ ID NO:12, 25, 14, 29, 31, 19, 21, 23 and 27, respectively).

DETAILED DESCRIPTION OF THE INVENTION

- 5 The present invention provides a growth and differentiation factor, GDF-8 and a polynucleotide sequence encoding GDF-8. GDF-8 is expressed at highest levels in muscle and at lower levels in adipose tissue.

The animals contemplated for use in the practice of the subject invention are those animals generally regarded as useful for the processing of food stuffs, *i.e.* avian such as
10 meat bred and egg laying chicken and turkey, ovine such as lamb, bovine such as beef cattle and milk cows, piscine and porcine. For purposes of the subject invention, these animals are referred to as "transgenic" when such animal has had a heterologous DNA sequence, or one or more additional DNA sequences normally endogenous to the animal (collectively referred to herein as "transgenes") chromosomally integrated into the germ
15 cells of the animal. The transgenic animal (including its progeny) will also have the transgene integrated into the chromosomes of somatic cells.

The TGF- β superfamily consists of multifunctional polypeptides that control proliferation, differentiation, and other functions in many cell types. Many of the peptides have regulatory, both positive and negative, effects on other peptide growth factors. The
20 structural homology between the GDF-8 protein of this invention and the members of the TGF- β family, indicates that GDF-8 is a new member of the family of growth and differentiation factors. Based on the known activities of many of the other members, it can be expected that GDF-8 will also possess biological activities that will make it useful as a diagnostic and therapeutic reagent.

- 25 In particular, certain members of this superfamily have expression patterns or possess activities that relate to the function of the nervous system. For example, the inhibins and

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activins have been shown to be expressed in the brain (Meunier, *et al.*, *Proc. Natl. Acad. Sci., USA*, 85:247, 1988; Sawchenko, *et al.*, *Nature*, 334:615, 1988), and activin has been shown to be capable of functioning as a nerve cell survival molecule (Schubert, *et al.*, *Nature*, 344:868, 1990). Another family member, namely, GDF-1, is nervous system-specific in its expression pattern (Lee, S.J., *Proc. Natl. Acad. Sci., USA*, 88:4250, 1991), and certain other family members, such as Vgr-1 (Lyons, *et al.*, *Proc. Natl. Acad. Sci., USA*, 86:4554, 1989; Jones, *et al.*, *Development*, 111:531, 1991), OP-1 (Ozkaynak, *et al.*, *J. Biol. Chem.*, 267:25220, 1992), and BMP-4 (Jones, *et al.*, *Development*, 111:531, 1991), are also known to be expressed in the nervous system. Because it is known that skeletal muscle produces a factor or factors that promote the survival of motor neurons (Brown, *Trends Neurosci.*, 7:10, 1984), the expression of GDF-8 in muscle suggests that one activity of GDF-8 may be as a trophic factor for neurons. In this regard, GDF-8 may have applications in the treatment of neurodegenerative diseases, such as amyotrophic lateral sclerosis or muscular dystrophy, or in maintaining cells or tissues in culture prior to transplantation.

GDF-8 may also have applications in treating disease processes involving muscle, such as in musculodegenerative diseases or in tissue repair due to trauma. In this regard, many other members of the TGF- β family are also important mediators of tissue repair. TGF- β has been shown to have marked effects on the formation of collagen and to cause a striking angiogenic response in the newborn mouse (Roberts, *et al.*, *Proc. Natl. Acad. Sci., USA* 83:4167, 1986). TGF- β has also been shown to inhibit the differentiation of myoblasts in culture (Massague, *et al.*, *Proc. Natl. Acad. Sci., USA* 83:8206, 1986). Moreover, because myoblast cells may be used as a vehicle for delivering genes to muscle for gene therapy, the properties of GDF-8 could be exploited for maintaining cells prior to transplantation or for enhancing the efficiency of the fusion.

The expression of GDF-8 in adipose tissue also raises the possibility of applications for GDF-8 in the treatment of obesity or of disorders related to abnormal proliferation of adipocytes. In this regard, TGF- β has been shown to be a potent inhibitor of adipocyte

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differentiation *in vitro* (Ignatz and Massague, *Proc. Natl. Acad. Sci., USA* 82:8530, 1985).

Polypeptides, Polynucleotides, Vectors and Host Cells

The invention provides substantially pure GDF-8 polypeptide and isolated polynucleo-
5 tides that encode GDF-8. The term "substantially pure" as used herein refers to GDF-8
which is substantially free of other proteins, lipids, carbohydrates or other materials with
which it is naturally associated. One skilled in the art can purify GDF-8 using standard
techniques for protein purification. The substantially pure polypeptide will yield a single
major band on a non-reducing polyacrylamide gel. The purity of the GDF-8 polypeptide
10 can also be determined by amino-terminal amino acid sequence analysis. GDF-8
polypeptide includes functional fragments of the polypeptide, as long as the activity of
GDF-8 remains. Smaller peptides containing the biological activity of GDF-8 are
included in the invention.

The invention provides polynucleotides encoding the GDF-8 protein. These polynucleo-
15 tides include DNA, cDNA and RNA sequences which encode GDF-8. It is understood
that all polynucleotides encoding all or a portion of GDF-8 are also included herein, as
long as they encode a polypeptide with GDF-8 activity. Such polynucleotides include
naturally occurring, synthetic, and intentionally manipulated polynucleotides. For
example, GDF-8 polynucleotide may be subjected to site-directed mutagenesis. The
20 polynucleotide sequence for GDF8 also includes antisense sequences. The polynucleo-
tides of the invention include sequences that are degenerate as a result of the genetic
code. There are 20 natural amino acids, most of which are specified by more than one
codon. Therefore, all degenerate nucleotide sequences are included in the invention as
long as the amino acid sequence of GDF-8 polypeptide encoded by the nucleotide
25 sequence is functionally unchanged.

Specifically disclosed herein is a genomic DNA sequence containing a portion of the
GDF-8 gene. The sequence contains an open reading frame corresponding to the
predicted C-terminal region of the GDF-8 precursor protein. The encoded polypeptide

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is predicted to contain two potential proteolytic processing sites (KR and RR). Cleavage of the precursor at the downstream site would generate a mature biologically active C-terminal fragment of 109 and 103 amino acids for murine and human species, respectively, with a predicted molecular weight of approximately 12,400. Also disclosed
5 are full length murine and human GDF-8 cDNA sequences. The murine pre-pro-GDF-8 protein is 376 amino acids in length, which is encoded by a 2676 base pair nucleotide sequence, beginning at nucleotide 104 and extending to a TGA stop codon at nucleotide 1232. The human GDF-8 protein is 375 amino acids and is encoded by a 2743 base pair sequence, with the open reading frame beginning at nucleotide 59 and extending to
10 nucleotide 1184. GDF-8 is also capable of forming dimers, or heterodimers, with an expected molecular weight of approximately 23-30KD (see Example 4). For example, GDF-8 may form heterodimers with other family members, such as GDF-11.

Also provided herein are the biologically active C-terminal fragments of chicken (Figure 2c) and rat (Figure 2d) GDF-8. The full length nucleotide and deduced amino acid
15 sequences for baboon, bovine, chicken, rat, ovine, porcine, and turkey are shown in Figures 14a-g and human and murine are shown in Figure 5. As shown in Figure 3b, alignment of the amino acid sequences of human, murine, rat and chicken GDF-8 indicate that the sequences are 100% identical in the C-terminal biologically active fragment. Figure 15 a and 15b also show the alignment of GDF-8 amino acid sequences
20 for murine, rat, human, baboon, porcine, ovine, bovine, chicken and turkey. Given the extensive conservation of amino acid sequences between species, it would now be routine for one of skill in the art to obtain the GDF-8 nucleic acid and amino acid sequence for GDF-8 from any species, including those provided herein, as well as piscine, for example.

25 The C-terminal region of GDF-8 following the putative proteolytic processing site shows significant homology to the known members of the TGF- β superfamily. The GDF-8 sequence contains most of the residues that are highly conserved in other family members and in other species (see FIGURES 3a and 3b and 15 a and 15b). Like the TGF- β s and inhibin β s, GDF-8 contains an extra pair of cysteine residues in addition to

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the 7 cysteines found in virtually all other family members. Among the known family members, GDF-8 is most homologous to Vgr-1 (45% sequence identity) (see FIGURE 4).

Minor modifications of the recombinant GDF-8 primary amino acid sequence may result in proteins which have substantially equivalent activity as compared to the GDF-8 polypeptide described herein. Such modifications may be deliberate, as by site-directed mutagenesis, or may be spontaneous. All of the polypeptides produced by these modifications are included herein as long as the biological activity of GDF-8 still exists. Further, deletion of one or more amino acids can also result in a modification of the structure of the resultant molecule without significantly altering its biological activity. This can lead to the development of a smaller active molecule which would have broader utility. For example, one can remove amino or carboxy terminal amino acids which are not required for GDF-8 biological activity.

The nucleotide sequence encoding the GDF-8 polypeptide of the invention includes the disclosed sequence and conservative variations thereof. The term "conservative variation" as used herein denotes the replacement of an amino acid residue by another, biologically similar residue. Examples of conservative variations include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine, and the like. The term "conservative variation" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid provided that antibodies raised to the substituted polypeptide also immunoreact with the unsubstituted polypeptide.

DNA sequences of the invention can be obtained by several methods. For example, the DNA can be isolated using hybridization techniques which are well known in the art. These include, but are not limited to: 1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences, 2) polymerase chain reaction (PCR) on genomic DNA or cDNA using primers capable of annealing to the DNA sequence of

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interest, and 3) antibody screening of expression libraries to detect cloned DNA fragments with shared structural features.

Preferably the GDF-8 polynucleotide of the invention is derived from a mammalian organism, and most preferably from mouse, rat, cow, pig, or human. GDF-8 polynucleo-
5 tides from chicken, turkey, fish and other species are also included herein. Screening procedures which rely on nucleic acid hybridization make it possible to isolate any gene sequence from any organism, provided the appropriate probe is available. Given the extensive nucleotide and amino acid homology between species, it would be routine for one of skill in the art to obtain polynucleotides encoding GDF-8 from any species. -
10 Oligonucleotide probes, which correspond to a part of the sequence encoding the protein in question, can be synthesized chemically. This requires that short, oligopeptide stretches of amino acid sequence must be known. The DNA sequence encoding the protein can be deduced from the genetic code, however, the degeneracy of the code must be taken into account. It is possible to perform a mixed addition reaction when the
15 sequence is degenerate. This includes a heterogeneous mixture of denatured double-stranded DNA. For such screening, hybridization is preferably performed on either single-stranded DNA or denatured double-stranded DNA. Hybridization is particularly useful in the detection of cDNA clones derived from sources where an extremely low amount of mRNA sequences relating to the polypeptide of interest are present. In other
20 words, by using stringent hybridization conditions directed to avoid non-specific binding, it is possible, for example, to allow the autoradiographic visualization of a specific cDNA clone by the hybridization of the target DNA to that single probe in the mixture which is its complete complement (Wallace, *et al.*, *Nucl. Acid Res.* 9:879, 1981).

The development of specific DNA sequences encoding GDF-8 can also be obtained by:
25 1) isolation of double-stranded DNA sequences from the genomic DNA; 2) chemical manufacture of a DNA sequence to provide the necessary codons for the polypeptide of interest; and 3) *in vitro* synthesis of a doublestranded DNA sequence by reverse transcription of mRNA isolated from a eukaryotic donor cell. In the latter case, a

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double-stranded DNA complement of mRNA is eventually formed which is generally referred to as cDNA.

Of the three above-noted methods for developing specific DNA sequences for use in recombinant procedures, the isolation of genomic DNA isolates is the least common.

- 5 This is especially true when it is desirable to obtain the microbial expression of mammalian polypeptides due to the presence of introns.

- The synthesis of DNA sequences is frequently the method of choice when the entire sequence of amino acid residues of the desired polypeptide product is known. When the entire sequence of amino acid residues of the desired polypeptide is not known, the direct
- 10 synthesis of DNA sequences is not possible and the method of choice is the synthesis of cDNA sequences. Among the standard procedures for isolating cDNA sequences of interest is the formation of plasmid- or phage-carrying cDNA libraries which are derived from reverse transcription of mRNA which is abundant in donor cells that have a high level of genetic expression. When used in combination with polymerase chain reaction
- 15 technology, even rare expression products can be cloned. In those cases where significant portions of the amino acid sequence of the polypeptide are known, the production of labeled single or double-stranded DNA or RNA probe sequences duplicating a sequence putatively present in the target cDNA may be employed in DNA/DNA hybridization procedures which are carried out on cloned copies of the cDNA which have been
- 20 denatured into a single-stranded form (Jay, *et al.*, *Nucl. Acid Res.*, 11:2325, 1983).

A cDNA expression library, such as lambda gt11, can be screened indirectly for GDF-8 peptides having at least one epitope, using antibodies specific for GDF-8. Such antibodies can be either polyclonally or monoclonally derived and used to detect expression product indicative of the presence of GDF-8 cDNA.

- 25 In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized. For example, the length, degree of complementarity, nucleotide sequence composition

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(*e.g.*, GC v. AT content), and nucleic acid type (*e.g.*, RNA v. DNA) of the hybridizing regions of the nucleic acids can be considered in selecting hybridization conditions. An additional consideration is whether one of the nucleic acids is immobilized, for example, on a filter.

- 5 An example of progressively higher stringency conditions is as follows: 2 x SSC/0.1% SDS at about room temperature (hybridization conditions); 0.2 x SSC/0.1% SDS at about room temperature (low stringency conditions); 0.2 x SSC/0.1% SDS at about 42°C (moderate stringency conditions); and 0.1 x SSC at about 68°C (high stringency conditions). Washing can be carried out using only one of these conditions, *e.g.*, high
10 stringency conditions, or each of the conditions can be used, *e.g.*, for 10-15 minutes each, in the order listed above, repeating any or all of the steps listed. However, as mentioned above, optimal conditions will vary, depending on the particular hybridization reaction involved, and can be determined empirically.

DNA sequences encoding GDF-8 can be expressed *in vitro* by DNA transfer into a
15 suitable host cell. "Host cells" are cells in which a vector can be propagated and its DNA expressed. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used. Methods of stable transfer, meaning that the foreign DNA is continuously
20 maintained in the host, are known in the art.

In the present invention, the GDF-8 polynucleotide sequences may be inserted into a recombinant expression vector. The term "recombinant expression vector" refers to a plasmid, virus or other vehicle known in the art that has been manipulated by insertion or incorporation of the GDF-8 genetic sequences. Such expression vectors contain a
25 promoter sequence which facilitates the efficient transcription of the inserted genetic sequence of the host. The expression vector typically contains an origin of replication, a promoter, as well as specific genes which allow phenotypic selection of the transformed cells. Vectors suitable for use in the present invention include, but are not limited

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to the T7-based expression vector for expression in bacteria (Rosenberg, *et al.*, *Gene*, 56:125, 1987), the pMSXND expression vector for expression in mammalian cells (Lee and Nathans, *J. Biol. Chem.*, 263:3521, 1988) and baculovirus-derived vectors for expression in insect cells. The DNA segment can be present in the vector operably linked
5 to regulatory elements, for example, a promoter (*e.g.*, T7, metallothionein I, or polyhedrin promoters).

Polynucleotide sequences encoding GDF-8 can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in
10 prokaryotes are well known in the art. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art. Such vectors are used to incorporate DNA sequences of the invention. Preferably, the mature C-terminal region of GDF-8 is expressed from a cDNA clone containing the entire coding sequence of GDF-8. Alternatively, the C-terminal portion of GDF-8 can be
15 expressed as a fusion protein with the pro- region of another member of the TGF- β family or co-expressed with another pro-region (see for example, Hammonds, *et al.*, *Molec. Endocrin.*, 5:149, 1991; Gray, A., and Mason, A., *Science*, 247:1328, 1990).

Transformation of a host cell with recombinant DNA may be carried out by conventional techniques as are well known to those skilled in the art. Where the host is prokaryotic,
20 such as *E. coli*, competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the CaCl_2 method using procedures well known in the art. Alternatively, MgCl_2 or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired.

25 When the host is a eukaryote, such methods of transfection of DNA as calcium phosphate co-precipitates, conventional mechanical procedures such as microinjection, electroporation, insertion of a plasmid encased in liposomes, or virus vectors may be used. Eukaryotic cells can also be cotransformed with DNA sequences encoding the GDF-8

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of the invention, and a second foreign DNA molecule encoding a selectable phenotype, such as the herpes simplex thymidine kinase gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 (SV40) or bovine papilloma virus, to transiently infect or transform eukaryotic cells and express the protein. (see for example, *Eukaryotic*
5 *Viral Vectors*, Cold Spring Harbor Laboratory, Gluzman ed., 1982).

Isolation and purification of microbial expressed polypeptide, or fragments thereof, provided by the invention, may be carried out by conventional means including preparative chromatography and immunological separations involving monoclonal or polyclonal antibodies.

10 GDF-8 Antibodies and Methods of Use

The invention includes antibodies immunoreactive with GDF-8 polypeptide or functional fragments thereof. Antibody which consists essentially of pooled monoclonal antibodies with different epitopic specificities, as well as distinct monoclonal antibody preparations are provided. Monoclonal antibodies are made from antigen containing fragments of the
15 protein by methods well known to those skilled in the art (Kohler, *et al.*, *Nature*, 256:495, 1975). The term antibody as used in this invention is meant to include intact molecules as well as fragments thereof, such as Fab and F(ab')₂, Fv and SCA fragments which are capable of binding an epitopic determinant on GDF-8.

(1) An Fab fragment consists of a monovalent antigen-binding fragment of an antibody
20 molecule, and can be produced by digestion of a whole antibody molecule with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain.

(2) An Fab' fragment of an antibody molecule can be obtained by treating a whole antibody molecule with pepsin, followed by reduction, to yield a molecule consisting of
25 an intact light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

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(3) An (Fab')₂ fragment of an antibody can be obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. A (Fab')₂ fragment is a dimer of two Fab' fragments, held together by two disulfide bonds.

(4) An Fv fragment is defined as a genetically engineered fragment containing the variable region of a light chain and the variable region of a heavy chain expressed as two chains.

(5) A single chain antibody ("SCA") is a genetically engineered single chain molecule containing the variable region of a light chain and the variable region of a heavy chain, linked by a suitable, flexible polypeptide linker.

10 As used in this invention, the term "epitope" refers to an antigenic determinant on an antigen, such as a GDF-8 polypeptide, to which the paratope of an antibody, such as an GDF-8-specific antibody, binds. Antigenic determinants usually consist of chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three-dimensional structural characteristics, as well as specific charge
15 characteristics.

As is mentioned above, antigens that can be used in producing GDF-8-specific antibodies include GDF-8 polypeptides or GDF-8 polypeptide fragments. The polypeptide or peptide used to immunize an animal can be obtained by standard recombinant, chemical synthetic, or purification methods. As is well known in the art, in order to increase
20 immunogenicity, an antigen can be conjugated to a carrier protein. Commonly used carriers include keyhole limpet hemocyanin (KLH), thyroglobulin, bovine serum albumin (BSA), and tetanus toxoid. The coupled peptide is then used to immunize the animal (e.g., a mouse, a rat, or a rabbit). In addition to such carriers, well known adjuvants can be administered with the antigen to facilitate induction of a strong immune response.

25 The term "cell-proliferative disorder" denotes malignant as well as non-malignant cell populations which often appear to differ from the surrounding tissue both morphologi-

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cally and genotypically. Malignant cells (*i.e.* cancer) develop as a result of a multistep process. The GDF-8 polynucleotide that is an antisense molecule or that encodes a dominant negative GDF-8 is useful in treating malignancies of the various organ systems, particularly, for example, cells in muscle or adipose tissue. Essentially, any disorder
5 which is etiologically linked to altered expression of GDF-8 could be considered susceptible to treatment with a GDF-8 agent (*e.g.*, a suppressing or enhancing agent). One such disorder is a malignant cell proliferative disorder, for example.

The invention provides a method for detecting a cell proliferative disorder of muscle or adipose tissue which comprises contacting an anti-GDF-8 antibody with a cell suspected
10 of having a GDF-8 associated disorder and detecting binding to the antibody. The antibody reactive with GDF-8 is labeled with a compound which allows detection of binding to GDF-8. For purposes of the invention, an antibody specific for GDF-8 polypeptide may be used to detect the level of GDF-8 in biological fluids and tissues. Any specimen containing a detectable amount of antigen can be used. A preferred sample
15 of this invention is muscle tissue. The level of GDF-8 in the suspect cell can be compared with the level in a normal cell to determine whether the subject has a GDF-8-associated cell proliferative disorder. Such methods of detection are also useful using nucleic acid hybridization to detect the level of GDF-8 mRNA in a sample or to detect an altered GDF-8 gene. Preferably the subject is human.

20 The antibodies of the invention can be used in any subject in which it is desirable to administer *in vitro* or *in vivo* immunodiagnosis or immunotherapy. The antibodies of the invention are suited for use, for example, in immunoassays in which they can be utilized in liquid phase or bound to a solid phase carrier. In addition, the antibodies in these immunoassays can be detectably labeled in various ways. Examples of types of
25 immunoassays which can utilize antibodies of the invention are competitive and non-competitive immunoassays in either a direct or indirect format. Examples of such immunoassays are the radioimmunoassay (RIA) and the sandwich (immunometric) assay. Detection of the antigens using the antibodies of the invention can be done utilizing immunoassays which are run in either the forward, reverse, or simultaneous modes,

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including immunohistochemical assays on physiological samples. Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

The antibodies of the invention can be bound to many different carriers and used to
5 detect the presence of an antigen comprising the polypeptide of the invention. Examples of well-known carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding
10 antibodies, or will be able to ascertain such, using routine experimentation.

There are many different labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds, and bioluminescent
15 compounds. Those of ordinary skill in the art will know of other suitable labels for binding to the antibody, or will be able to ascertain such, using routine experimentation.

Another technique which may also result in greater sensitivity consists of coupling the antibodies to low molecular weight haptens. These haptens can then be specifically detected by means of a second reaction. For example, it is common to use such haptens
20 as biotin, which reacts with avidin, or dinitrophenyl, puridoxal, and fluorescein, which can react with specific antihapten antibodies.

In using the monoclonal antibodies of the invention for the *in vivo* detection of antigen, the detectably labeled antibody is given a dose which is diagnostically effective. The term "diagnostically effective" means that the amount of detectably labeled monoclonal
25 antibody is administered in sufficient quantity to enable detection of the site having the antigen comprising a polypeptide of the invention for which the monoclonal antibodies are specific.

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The concentration of detectably labeled monoclonal antibody which is administered should be sufficient such that the binding to those cells having the polypeptide is detectable compared to the background. Further, it is desirable that the detectably labeled monoclonal antibody be rapidly cleared from the circulatory system in order to give the
5 best target-to-background signal ratio.

As a rule, the dosage of detectably labeled monoclonal antibody for *in vivo* diagnosis will vary depending on such factors as age, sex, and extent of disease of the individual. Such dosages may vary, for example, depending on whether multiple injections are given, antigenic burden, and other factors known to those of skill in the art.

10 For *in vivo* diagnostic imaging, the type of detection instrument available is a major factor in selecting a given radioisotope. The radioisotope chosen must have a type of decay which is detectable for a given type of instrument. Still another important factor in selecting a radioisotope for *in vivo* diagnosis is that deleterious radiation with respect to the host is minimized. Ideally, a radioisotope used for *in vivo* imaging will lack a
15 particle emission, but produce a large number of photons in the 140-250 keV range, which may readily be detected by conventional gamma cameras.

For *in vivo* diagnosis radioisotopes may be bound to immunoglobulin either directly or indirectly by using an intermediate functional group. intermediate functional groups which often are used to bind radioisotopes which exist as metallic ions to i-
20 mmunoglobulins are the bifunctional chelating agents such as diethylenetriaminepentaacetic acid (DTPA) and ethylenediaminetetraacetic acid (EDTA) and similar molecules. Typical examples of metallic ions which can be bound to the monoclonal antibodies of the invention are ^{111}In , ^{97}Ru , ^{67}Ga , ^{68}Ga , ^{72}As , ^{89}Zr and ^{201}Tl .

The monoclonal antibodies of the invention can also be labeled with a paramagnetic
25 isotope for purposes of *in vivo* diagnosis, as in magnetic resonance imaging (MRI) or electron spin resonance (ESR). In general, any conventional method for visualizing diagnostic imaging can be utilized. Usually gamma and positron emitting radioisotopes

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are used for camera imaging and paramagnetic isotopes for MRI. Elements which are particularly useful in such techniques include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Cr , and ^{56}Fe .

The monoclonal antibodies of the invention can be used *in vitro* and *in vivo* to monitor the course of amelioration of a GDF-8-associated disease in a subject. Thus, for example,
5 by measuring the increase or decrease in the number of cells expressing antigen comprising a polypeptide of the invention or changes in the concentration of such antigen present in various body fluids, it would be possible to determine whether a particular therapeutic regimen aimed at ameliorating the GDF-8-associated disease is effective. The term "ameliorate" denotes a lessening of the detrimental effect of the GDF-8-associated
10 disease in the subject receiving therapy.

Additional Methods of Treatment and Diagnosis

The present invention identifies a nucleotide sequence that can be expressed in an altered manner as compared to expression in a normal cell, therefore it is possible to design appropriate therapeutic or diagnostic techniques directed to this sequence. Treatment
15 includes administration of a reagent which modulates activity. The term "modulate" envisions the suppression or expression of GDF-8 when it is over-expressed, or augmentation of GDF-8 expression when it is underexpressed. When a muscle-associated disorder is associated with GDF-8 overexpression, such suppressive reagents as antisense GDF-8 polynucleotide sequence, dominant negative sequences or GDF-8
20 binding antibody can be introduced into a cell. In addition, an anti-idiotypic antibody which binds to a monoclonal antibody which binds GDF-8 of the invention, or an epitope thereof, may also be used in the therapeutic method of the invention. Alternatively, when a cell proliferative disorder is associated with underexpression or expression of a mutant GDF-8 polypeptide, a sense polynucleotide sequence (the DNA coding strand) or GDF-8
25 polypeptide can be introduced into the cell. Such muscle-associated disorders include cancer, muscular dystrophy, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia. One of skill in the art can determine whether or not a particular therapeutic course of treatment is successful by several methods described herein (e.g., muscle fiber analysis or biopsy). Neurodegenerative

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disorders are also envisioned as treated by the method of the invention. In addition, the method of the invention can be used in the treatment of obesity or of disorders related to abnormal proliferation of adipocytes. One of skill in the art can determine whether or not a particular therapeutic course of treatment is successful by several methods described
5 herein (e.g., muscle fiber analysis or biopsy; determination of fat content). The present examples demonstrate that the methods of the invention are useful for decreasing fat content, and therefore would be useful in the treatment of obesity and related disorders (e.g., diabetes). Neurodegenerative disorders are also envisioned as treated by the method of the invention.

10 Thus, where a cell-proliferative disorder is associated with the expression of GDF-8, nucleic acid sequences that interfere with GDF-8 expression at the translational level can be used. This approach utilizes, for example, antisense nucleic acid and ribozymes to block translation of a specific GDF-8 mRNA, either by masking that mRNA with an antisense nucleic acid or by cleaving it with a ribozyme. Such disorders include
15 neurodegenerative diseases, for example. In addition, dominant-negative GDF-8 mutants would be useful to actively interfere with function of "normal" GDF-8.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule (Weintraub, *Scientific American*, 262:40, 1990). In the cell, the antisense nucleic acids hybridize to the corresponding mRNA, forming
20 a double-stranded molecule. The antisense nucleic acids interfere with the translation of the mRNA, since the cell will not translate a mRNA that is double-stranded.

Antisense oligomers of about 15 nucleotides are preferred, since they are easily synthesized and are less likely to cause problems than larger molecules when introduced into the target GDF-8-producing cell. The use of antisense methods to inhibit the *in vitro*
25 translation of genes is well known in the art (Marcus-Sakura, *Anal. Biochem.*, 172:289, 1988).

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Ribozymes are RNA molecules possessing the ability to specifically cleave other single-stranded RNA in a manner analogous to DNA restriction endonucleases. Through the modification of nucleotide sequences which encode these RNAs, it is possible to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and
5 cleave it (Cech, *J. Amer. Med. Assn.*, 260:3030, 1988). A major advantage of this approach is that, because they are sequence-specific, only mRNAs with particular sequences are inactivated.

There are two basic types of ribozymes namely, tetrahymena-type (Hasselhoff, *Nature*, 334:585, 1988) and "hammerhead"-type. Tetrahymena-type ribozymes recognize
10 sequences which are four bases in length, while "hammerhead"-type ribozymes recognize base sequences 11-18 bases in length. The longer the recognition sequence, the greater the likelihood that the sequence will occur exclusively in the target mRNA species. Consequently, hammerhead-type ribozymes are preferable to tetrahymena-type ribozymes for inactivating a specific mRNA species and 18-based recognition sequences
15 are preferable to shorter recognition sequences.

In another embodiment of the present invention, a nucleotide sequence encoding a GDF-8 dominant negative protein is provided. For example, a genetic construct that contain such a dominant negative encoding gene may be operably linked to a promoter, such as a tissue-specific promoter. For example, a skeletal muscle specific promoter (*e.g.*,
20 human skeletal muscle α -actin promoter) or developmentally specific promoter (*e.g.*, MyHC 3, which is restricted in skeletal muscle to the embryonic period of development, or an inducible promoter (*e.g.*, the orphan nuclear receptor TIS1).

Such constructs are useful in methods of modulating a subject's skeletal mass. For example, a method include transforming an organism, tissue, organ or cell with a genetic
25 construct encoding a dominant negative GDF-8 protein and suitable promoter in operable linkage and expressing the dominant negative encoding GDF-8 gene, thereby modulating muscle mass by interfering with wild-type GDF-8 activity.

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- GDF-8 most likely forms dimers, homodimers or heterodimers and may even form heterodimers with other GDF family members, such as GDF-11 (*see* Example 4). Hence, while not wanting to be bound by a particular theory, the dominant negative effect described herein may involve the formation of non-functional homodimers or heterodimers of dominant negative and wild-type GDF-8 monomers. More specifically, it is possible that any non-functional homodimer or any heterodimer formed by the dimerization of wild-type and/or dominant negative GDF-8 monomers produces a dominant effect by: 1) being synthesized but not processed or secreted; 2) inhibiting the secretion of wild type GDF-8; 3) preventing normal proteolytic cleavage of the preprotein thereby producing a nonfunctional GDF-8 molecule; 4) altering the affinity of the non-functional dimer (e.g., homodimeric or heterodimeric GDF-8) to a receptor or generating an antagonistic form of GDF-8 that binds a receptor without activating it; or 5) inhibiting the intracellular processing or secretion of GDF-8 related or TGF- β family proteins.
- 15 Non-functional GDF-8 can function to inhibit the growth regulating actions of GDF-8 on muscle cells that include a dominant negative GDF-8 gene. Deletion or missense dominant negative forms of GDF-8 that retain the ability to form dimers with wild-type GDF-8 protein but do not function as wild-type GDF-8 proteins may be used to inhibit the biological activity of endogenous wild-type GDF-8. For example, in one embodiment, the proteolytic processing site of GDF-8 may be altered (e.g., deleted) resulting in a GDF-8 molecule able to undergo subsequent dimerization with endogenous wild-type GDF-8 but unable to undergo further processing into a mature GDF-8 form. Alternatively, a non-functional GDF-8 can function as a monomeric species to inhibit the growth regulating actions of GDF-8 on muscle cells.
- 25 Any genetic recombinant method in the art may be used, for example, recombinant viruses may be engineered to express a dominant negative form of GDF-8 which may be used to inhibit the activity of wild-type GDF-8. Such viruses may be used therapeutically for treatment of diseases resulting from aberrant over-expression or activity of GDF-8 protein, such as in denervation hypertrophy or as a means of

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controlling GDF-8 expression when treating disease conditions involving muscle, such as in musculodegenerative diseases or in tissue repair due to trauma or in modulating GDF-8 expression in animal husbandry (e.g., transgenic animals for agricultural purposes).

- 5 The invention provides a method for treating a muscle or adipose tissue disorder in a subject. The method includes administering a therapeutically effective amount of a GDF-8 agent to the subject, thereby inhibiting abnormal growth of muscle or adipose tissue. The GDF-8 agent may include a GDF-8 antisense molecule or a dominant negative polypeptide, for example. A "therapeutically effective amount" of a GDF-8
10 agent is that amount that ameliorates symptoms of the disorder or inhibits GDF-8 induced growth of muscle, for example, as compared with a normal subject.

Gene Therapy

- The present invention also provides gene therapy for the treatment of cell proliferative or immunologic disorders which are mediated by GDF-8 protein. Such therapy would
15 achieve its therapeutic effect by introduction of the GDF-8 antisense or dominant negative encoding polynucleotide into cells having the proliferative disorder. Delivery of antisense or dominant negative GDF-8 polynucleotide can be achieved using a recombinant expression vector such as a chimeric virus or a colloidal dispersion system. Especially preferred for therapeutic delivery of antisense or dominant negative sequences
20 is the use of targeted liposomes. In contrast, when it is desirable to enhance GDF-8 production, a "sense" GDF-8 polynucleotide or functional equivalent (e.g., the C-term active region) is introduced into the appropriate cell(s).

- Various viral vectors which can be utilized for gene therapy as taught herein include adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus.
25 Preferably, the retroviral vector is a derivative of a murine or avian retrovirus. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV).

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A number of additional retroviral vectors can incorporate multiple genes. All of these vectors can transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting a GDF-8 sequence of interest into the viral vector, along with another gene which encodes the ligand for a receptor on a specific target cell, for example, the vector is now target specific. Retroviral vectors can be made target specific by attaching, for example, a sugar, a glycolipid, or a protein. Preferred targeting is accomplished by using an antibody to target the retroviral vector. Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral genome or attached to a viral envelope to allow target specific delivery of the retroviral vector containing the GDF-8 antisense polynucleotide.

Since recombinant retroviruses are defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packaging mechanism to recognize an RNA transcript for encapsulation. Helper cell lines which have deletions of the packaging signal include, but are not limited to ψ 2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced.

Alternatively, NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes gag, pol and env, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium.

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Another targeted delivery system for GDF-8 polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles *in vitro* and *in vivo*. It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-4.0 μm can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, *et al.*, *Trends Biochem. Sci.*, 6:77, 1981). In addition to mammalian cells, liposomes have been used for delivery of polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high efficiency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Manning, *et al.*, *Biotechniques*, 6:682, 1988).

The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations.

Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerebroside, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative

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phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine.

The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to cells of the reticulo-endothelial system (RES) in organs which contain sinusoidal capillaries. Active targeting, on the other hand, involves alteration of the liposome by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein, or by changing the composition or size of the liposome in order to achieve targeting to organs and cell types other than the naturally occurring sites of localization.

The surface of the targeted delivery system may be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand.

Due to the expression of GDF-8 in muscle and adipose tissue, there are a variety of applications using the polypeptide, polynucleotide, and antibodies of the invention, related to these tissues. Such applications include treatment of cell proliferative disorders involving these and other tissues, such as neural tissue. In addition, GDF-8 may be useful in various gene therapy procedures. In embodiments where GDF-8 polypeptide is administered to a subject, the dosage range is about 0.1 ug/kg to 100 mg/kg; more preferably from about 1 ug/kg to 75 mg/kg and most preferably from about 10 mg/kg to 50 mg/kg.

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Chromosomal Location of GDF-8

The data in Example 6 shows that the human GDF-8 gene is located on chromosome 2. By comparing the chromosomal location of GDF-8 with the map positions of various human disorders, it should be possible to determine whether mutations in the GDF-8 gene are involved in the etiology of human diseases. For example, an autosomal recessive form of juvenile amyotrophic lateral sclerosis has been shown to map to chromosome 2 (Hentati, *et al.*, *Neurology*, 42 [Suppl.3]:201, 1992). More precise mapping of GDF-8 and analysis of DNA from these patients may indicate that GDF-8 is, in fact, the gene affected in this disease. In addition, GDF-8 is useful for distinguishing chromosome 2 from other chromosomes.

Transgenic Animals and Methods of Making the same

Various methods to make the transgenic animals of the subject invention can be employed. Generally speaking, three such methods may be employed. In one such method, an embryo at the pronuclear stage (a "one cell embryo") is harvested from a female and the transgene is microinjected into the embryo, in which case the transgene will be chromosomally integrated into both the germ cells and somatic cells of the resulting mature animal. In another such method, embryonic stem cells are isolated and the transgene incorporated therein by electroporation, plasmid transfection or microinjection, followed by reintroduction of the stem cells into the embryo where they colonize and contribute to the germ line. Methods for microinjection of mammalian species is described in United States Patent No. 4,873,191. In yet another such method, embryonic cells are infected with a retrovirus containing the transgene whereby the germ cells of the embryo have the transgene chromosomally integrated therein. When the animals to be made transgenic are avian, because avian fertilized ova generally go through cell division for the first twenty hours in the oviduct, microinjection into the pronucleus of the fertilized egg is problematic due to the inaccessibility of the pronucleus. Therefore, of the methods to make transgenic animals described generally above, retrovirus infection is preferred for avian species, for example as described in U.S. 5,162,215. If microinjection is to be used with avian species, however, a recently published procedure by Love *et al.*, (*Biotechnology*, 12, Jan 1994) can be utilized

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whereby the embryo is obtained from a sacrificed hen approximately two and one-half hours after the laying of the previous laid egg, the transgene is microinjected into the cytoplasm of the germinal disc and the embryo is cultured in a host shell until maturity. When the animals to be made transgenic are bovine or porcine, microinjection can be
5 hampered by the opacity of the ova thereby making the nuclei difficult to identify by traditional differential interference-contrast microscopy. To overcome this problem, the ova can first be centrifuged to segregate the pronuclei for better visualization.

The "non-human animals" of the invention bovine, porcine, ovine and avian animals (*e.g.*, cow, pig, sheep, chicken, turkey). The "transgenic non-human animals" of the
10 invention are produced by introducing "transgenes" into the germline of the non-human animal. Embryonal target cells at various developmental stages can be used to introduce transgenes. Different methods are used depending on the stage of development of the embryonal target cell. The zygote is the best target for micro-injection. The use of zygotes as a target for gene transfer has a major advantage in that in most cases the
15 injected DNA will be incorporated into the host gene before the first cleavage (Brinster *et al.*, *Proc. Natl. Acad. Sci. USA* 82:4438-4442, 1985). As a consequence, all cells of the transgenic non-human animal will carry the incorporated transgene. This will in general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene.

20 The term "transgenic" is used to describe an animal which includes exogenous genetic material within all of its cells. A "transgenic" animal can be produced by cross-breeding two chimeric animals which include exogenous genetic material within cells used in reproduction. Twenty-five percent of the resulting offspring will be transgenic *i.e.*, animals which include the exogenous genetic material within all of their cells in both
25 alleles. 50% of the resulting animals will include the exogenous genetic material within one allele and 25% will include no exogenous genetic material.

In the microinjection method useful in the practice of the subject invention, the transgene is digested and purified free from any vector DNA *e.g.* by gel electrophoresis. It is

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preferred that the transgene include an operatively associated promoter which interacts with cellular proteins involved in transcription, ultimately resulting in constitutive expression. Promoters useful in this regard include those from cytomegalovirus (CMV), Moloney leukemia virus (MLV), and herpes virus, as well as those from the genes
5 encoding metallothionin, skeletal actin, P-enolpyruvate carboxylase (PEPCK), phosphoglycerate (PGK), DHFR, and thymidine kinase. Promoters for viral long terminal repeats (LTRs) such as Rous Sarcoma Virus can also be employed. When the animals to be made transgenic are avian, preferred promoters include those for the chicken β -globin gene, chicken lysozyme gene, and avian leukosis virus. Constructs
10 useful in plasmid transfection of embryonic stem cells will employ additional regulatory elements well known in the art such as enhancer elements to stimulate transcription, splice acceptors, termination and polyadenylation signals, and ribosome binding sites to permit translation.

Retroviral infection can also be used to introduce transgene into a non-human animal, as
15 described above. The developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retro viral infection (Jaenich, R., Proc. Natl. Acad. Sci USA 73:1260-1264, 1976). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (Hogan, *et al.* (1986) in Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press,
20 Cold Spring Harbor, N.Y.). The viral vector system used to introduce the transgene is typically a replication-defective retro virus carrying the transgene (Jahner, *et al.*, Proc. Natl. Acad. Sci. USA 82:6927-6931, 1985; Van der Putten, *et al.*, Proc. Natl. Acad. Sci USA 82:6148-6152, 1985). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten, *supra*; Stewart,
25 *et al.*, EMBO J. 6:383-388, 1987). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (D. Jahner *et al.*, Nature 298:623-628, 1982). Most of the founders will be mosaic for the transgene since incorporation occurs only in a subset of the cells which formed the transgenic nonhuman animal. Further, the founder may contain various retro viral insertions of the transgene
30 at different positions in the genome which generally will segregate in the offspring. In

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addition, it is also possible to introduce transgenes into the germ line, albeit with low efficiency, by intrauterine retroviral infection of the midgestation embryo (D. Jahner *et al.*, *supra*).

A third type of target cell for transgene introduction is the embryonal stem cell (ES). ES
5 cells are obtained from pre-implantation embryos cultured *in vitro* and fused with
embryos (M. J. Evans *et al.* *Nature* 292:154-156, 1981; M.O. Bradley *et al.*, *Nature* 309:
255-258, 1984; Gossler, *et al.*, *Proc. Natl. Acad. Sci USA* 83: 9065-9069, 1986; and
Robertson *et al.*, *Nature* 322:445-448, 1986). Transgenes can be efficiently introduced
into the ES cells by DNA transfection or by retro virus-mediated transduction. Such
10 transformed ES cells can thereafter be combined with blastocysts from a nonhuman
animal. The ES cells thereafter colonize the embryo and contribute to the germ line of
the resulting chimeric animal. (For review see Jaenisch, R., *Science* 240: 1468-1474,
1988).

"Transformed" means a cell into which (or into an ancestor of which) has been
15 introduced, by means of recombinant nucleic acid techniques, a heterologous nucleic acid
molecule. "Heterologous" refers to a nucleic acid sequence that either originates from
another species or is modified from either its original form or the form primarily
expressed in the cell.

"Transgene" means any piece of DNA which is inserted by artifice into a cell, and
20 becomes part of the genome of the organism (*i.e.*, either stably integrated or as a stable
extrachromosomal element) which develops from that cell. Such a transgene may
include a gene which is partly or entirely heterologous (*i.e.*, foreign) to the transgenic
organism, or may represent a gene homologous to an endogenous gene of the organism.
Included within this definition is a transgene created by the providing of an RNA
25 sequence which is transcribed into DNA and then incorporated into the genome. The
transgenes of the invention include DNA sequences which encode GDF-8, and include
GDF-sense, antisense, dominant negative encoding polynucleotides, which may be
expressed in a transgenic non-human animal. The term "transgenic" as used herein

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additionally includes any organism whose genome has been altered by *in vitro* manipulation of the early embryo or fertilized egg or by any transgenic technology to induce a specific gene knockout. The term "gene knockout" as used herein, refers to the targeted disruption of a gene *in vivo* with complete loss of function that has been
5 achieved by any transgenic technology familiar to those in the art. In one embodiment, transgenic animals having gene knockouts are those in which the target gene has been rendered nonfunctional by an insertion targeted to the gene to be rendered non-functional by homologous recombination. As used herein, the term "transgenic" includes any transgenic technology familiar to those in the art which can produce an organism
10 carrying an introduced transgene or one in which an endogenous gene has been rendered non-functional or "knocked out." An example of a transgene used to "knockout" GDF-8 function in the present Examples is described in Example 8 and FIGURE 12a. Thus, in another embodiment, the invention provides a transgene wherein the entire mature C-terminal region of GDF-8 is deleted.

15 The transgene to be used in the practice of the subject invention is a DNA sequence comprising a modified GDF-8 coding sequence. In a preferred embodiment, the GDF-8 gene is disrupted by homologous targeting in embryonic stem cells. For example, the entire mature C-terminal region of the GDF-8 gene may be deleted as described in the examples below. Optionally, the GDF-8 disruption or deletion may be accompanied by
20 insertion of or replacement with other DNA sequences, such as a non-functional GDF-8 sequence. In other embodiments, the transgene comprises DNA antisense to the coding sequence for GDF-8. In another embodiment, the transgene comprises DNA encoding an antibody or receptor peptide sequence which is able to bind to GDF-8. The DNA and peptide sequences of GDF-8 are known in the art, the sequences, localization and activity
25 disclosed in WO94/21681 and pending United States patent application 08/033,923, filed on March 19, 1993, incorporated by reference in its entirety. The disclosure of both of these applications are hereby incorporated herein by reference. Where appropriate, DNA sequences that encode proteins having GDF-8 activity but differ in nucleic acid sequence due to the degeneracy of the genetic code may also be used herein, as may truncated
30 forms, allelic variants and interspecies homologues.

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The invention also includes animals having heterozygous mutations in GDF-8 or partial inhibition of GDF-8 function or expression. A heterozygote would exhibit an intermediate increase in muscle mass as compared to the homozygote as shown in Table 4 below. In other words, partial loss of function leads to a partial increase in muscle mass. One of skill in the art would readily be able to determine if a particular mutation or if an antisense molecule was able to partially inhibit GDF-8. For example, *in vitro* testing may be desirable initially by comparison with wild-type or untreated GDF-8 (*e.g.*, comparison of northern blots to examine a decrease in expression).

After an embryo has been microinjected, colonized with transfected embryonic stem cells or infected with a retrovirus containing the transgene (except for practice of the subject invention in avian species which is addressed elsewhere herein) the embryo is implanted into the oviduct of a pseudopregnant female. The consequent progeny are tested for incorporation of the transgene by Southern blot analysis of blood samples using transgene specific probes. PCR is particularly useful in this regard. Positive progeny (G0) are crossbred to produce offspring (G1) which are analyzed for transgene expression by Northern blot analysis of tissue samples. To be able to distinguish expression of like-species transgenes from expression of the animals endogenous GDF-8 gene(s), a marker gene fragment can be included in the construct in the 3' untranslated region of the transgene and the Northern probe designed to probe for the marker gene fragment. The serum levels of GDF-8 can also be measured in the transgenic animal to establish appropriate expression. Expression of the GDF-8 transgenes, thereby decreasing the GDF-8 in the tissue and serum levels of the transgenic animals and consequently increasing the muscle tissue content results in the foodstuffs from these animals (*i.e.* eggs, beef, pork, poultry meat, milk, *etc.*) having markedly increased muscle content, and preferably without increased, and more preferably, reduced levels of fat and cholesterol. By practice of the subject invention, a statistically significant increase in muscle content, preferably at least a 2% increase in muscle content (*e.g.*, in chickens), more preferably a 25% increase in muscle content as a percentage of body weight, more preferably greater than 40% increase in muscle content in these foodstuffs can be obtained.

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Additional Methods of Use

Thus, the present invention includes methods for increasing muscle mass in domesticated animals, characterized by inactivation or deletion of the gene encoding growth and differentiation factor-8 (GDF-8). The domesticated animal is preferably selected from the group consisting of ovine, bovine, porcine, piscine and avian. The animal may be treated with an isolated polynucleotide sequence encoding growth and differentiation factor-8 which polynucleotide sequence is also from a domesticated animal selected from the group consisting of ovine, bovine, porcine, piscine and avian. The present invention includes methods for increasing the muscle mass in domesticated animals characterized by administering to a domesticated animal monoclonal antibodies directed to the GDF-8 polypeptide. The antibody may be an anti-GDF-8, and may be either a monoclonal antibody or a polyclonal antibody.

The invention includes methods comprising using an anti-GDF-8 monoclonal antibody, antisense, or dominant negative mutants as a therapeutic agent to inhibit the growth regulating actions of GDF-8 on muscle cells. Muscle cells are defined to include fetal or adult muscle cells, as well as progenitor cells which are capable of differentiation into muscle. The monoclonal antibody may be a humanized (*e.g.*, either fully or a chimeric) monoclonal antibody, of any species origin, such as murine, ovine, bovine, porcine or avian. Methods of producing antibody molecules with various combinations of "humanized" antibodies are well known in the art and include combining murine variable regions with human constant regions (Cabily, *et al. Proc.Natl.Acad.Sci. USA*, 81:3273, 1984), or by grafting the murine-antibody complementary determining regions (CDRs) onto the human framework (Richmann, *et al., Nature* 332:323, 1988). Other general references which teach methods for creating humanized antibodies include Morrison, *et al., Science*, 229:1202, 1985; Jones, *et al., Nature*, 321:522, 1986; Monroe, *et al., Nature* 312:779, 1985; Oi, *et al., BioTechniques*, 4:214, 1986; European Patent Application No. 302,620; and U.S. Patent No. 5,024,834. Therefore, by humanizing the monoclonal antibodies of the invention for *in vivo* use, an immune response to the antibodies would be greatly reduced.

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The monoclonal antibody, GDF-8 polypeptide, or GDF-8 polynucleotide (all "GDF-8 agents") may have the effect of increasing the development of skeletal muscles. In preferred embodiments of the claimed methods, the GDF-8 monoclonal antibody, polypeptide, or polynucleotide is administered to a patient suffering from a disorder
5 selected from the group consisting of muscle wasting disease, neuromuscular disorder, muscle atrophy or aging. The GDF-8 agent may also be administered to a patient suffering from a disorder selected from the group consisting of muscular dystrophy, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia. In a preferred embodiment, the GDF-8 agent is administered to a
10 patient with muscle wasting disease or disorder by intravenous, intramuscular or subcutaneous injection; preferably, a monoclonal antibody is administered within a dose range between about 0.1 mg/kg to about 100 mg/kg; more preferably between about 1 ug/kg to 75 mg/kg; most preferably from about 10 mg/kg to 50 mg/kg. The antibody may be administered, for example, by bolus injection or by slow infusion. Slow
15 infusion over a period of 30 minutes to 2 hours is preferred. The GDF-8 agent may be formulated in a formulation suitable for administration to a patient. Such formulations are known in the art.

The dosage regimen will be determined by the attending physician considering various factors which modify the action of the GDF-8 protein, *e.g.* amount of tissue desired to
20 be formed, the site of tissue damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue, the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and the types of agent, such as anti-GDF-8 antibodies, to be used in the composition. Generally, systemic or injectable administra-
25 tion, such as intravenous (IV), intramuscular (IM) or subcutaneous (Sub-Q) injection. Administration will generally be initiated at a dose which is minimally effective, and the dose will be increased over a preselected time course until a positive effect is observed. Subsequently, incremental increases in dosage will be made limiting such incremental increases to such levels that produce a corresponding increase in effect, while taking into
30 account any adverse affects that may appear. The addition of other known growth

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factors, such as IGF I (insulin like growth factor I), human, bovine, or chicken growth hormone which may aid in increasing muscle mass, to the final composition, may also affect the dosage. In the embodiment where an anti-GDF-8 antibody is administered, the anti-GDF-8 antibody is generally administered within a dose range of about 0.1 ug/kg
5 to about 100 mg/kg.; more preferably between about 10 mg/kg to 50 mg/kg.

Progress can be monitored by periodic assessment of tissue growth and/or repair. The progress can be monitored, for example, x-rays, histomorphometric determinations and tetracycline labeling.

Screening for GDF-8 Modulating Compounds

- 10 In another embodiment, the invention provides a method for identifying a compound or molecule that modulates GDF-8 protein activity or gene expression. The method includes incubating components comprising the compound, GDF-8 polypeptide or with a recombinant cell expressing GDF-8 polypeptide, under conditions sufficient to allow the components to interact and determining the effect of the compound on GDF-8
15 activity or expression. The effect of the compound on GDF-8 activity can be measured by a number of assays, and may include measurements before and after incubating in the presence of the compound. Compounds that affect GDF-8 activity or gene expression include peptides, peptidomimetics, polypeptides, chemical compounds and biologic agents. Assays include Northern blot analysis of GDF-8 mRNA (for gene expression),
20 Western blot analysis (for protein level) and muscle fiber analysis (for protein activity).

The above screening assays may be used for detecting the compounds or molecules that bind to the GDF-8 receptor or GDF-8 polypeptide, in isolating molecules that bind to the GDF-8 gene, for measuring the amount of GDF-8 in a sample, either polypeptide or RNA (mRNA), for identifying molecules that may act as agonists or antagonists, and the like.
25 For example, GDF-8 antagonists are useful for treatment of muscular and adipose tissue disorders (e.g., obesity).

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Incubating includes conditions which allow contact between the test compound and GDF-8 polypeptide or with a recombinant cell expressing GDF-8 polypeptide. Contacting includes in solution and in solid phase, or in a cell. The test compound may optionally be a combinatorial library for screening a plurality of compounds. Compounds identified in the method of the invention can be further evaluated, detected, cloned, sequenced, and the like, either in solution or after binding to a solid support, by any method usually applied to the detection of a specific DNA sequence such as PCR, oligomer restriction (Saiki, *et al.*, *Bio/Technology*, 3:1008-1012, 1985), allele-specific oligonucleotide (ASO) probe analysis (Conner, *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:278, 1983), oligonucleotide Landegren, *et al.*, *Science*, 241:1077, 1988), and the like. Molecular techniques for DNA analysis have been reviewed (Landegren, *et al.*, *Science*, 242:229-237, 1988).

All references cited herein are hereby incorporated by reference in their entirety.

The following examples are intended to illustrate but not limit the invention. While they are typical of those that might be used, other procedures known to those skilled in the art may alternatively be used.

EXAMPLE 1

IDENTIFICATION AND ISOLATION OF A NOVEL

TGF- β FAMILY MEMBER

To identify a new member of the TGF- β superfamily, degenerate oligonucleotides were designed which corresponded to two conserved regions among the known family members: one region spanning the two tryptophan residues conserved in all family members except MIS and the other region spanning the invariant cysteine residues near the C-terminus. These primers were used for polymerase chain reactions on mouse genomic DNA followed by subcloning the PCR products using restriction sites placed at the 5' ends of the primers, picking individual *E. coli* colonies carrying these subcloned

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inserts, and using a combination of random sequencing and hybridization analysis to eliminate known members of the superfamily.

GDF-8 was identified from a mixture of PCR products obtained with the primers

SJL141: 5'-CCGGAATTCGGITGG(G/C/A)A(G/A/T/C)(A/G)A(T/C)TGG(A/G)TI

5 (A/G)TI(T/G)CICC-3' (SEQ ID NO:1)

SJL147:

5'-CCGGAATTC(G/A)CAI(G/C)C(G/A)CA(G/A)CT(G/A/T/C)

TCIACI(G/A)(T/C)CAT-3' (SEQ ID NO:2)

PCR using these primers was carried out with 2 µg mouse genomic DNA at 94°C for 1
10 min, 50°C for 2 min, and 72°C for 2 min for 40 cycles.

PCR products of approximately 280 bp were gel-purified, digested with Eco RI, gel-purified again, and subcloned in the Bluescript vector (Stratagene, San Diego, CA). Bacterial colonies carrying individual subclones were picked into 96 well microtiter plates, and multiple replicas were prepared by plating the cells onto nitrocellulose. The
15 replicate filters were hybridized to probes representing known members of the family, and DNA was prepared from nonhybridizing colonies for sequence analysis.

The primer combination of SJL141 and SJL147, encoding the amino acid sequences GW(H/Q/N/K/D/E)(D/N)W(V/I/M)(V/I/M)(A/S)P (SEQ ID NO:9) and M(V/I/M/T/A)V(D/E)SC(G/A)C (SEQ ID NO:10), respectively, yielded four previously
20 identified sequences (BMP-4, inhibin, βB, GDF-3 and GDF-5) and one novel sequence, which was designated GDF-8, among 110 subclones analyzed.

Human GDF-8 was isolated using the primers:

ACM13: 5'-CGCGGATCCAGAGTCAAGGTGACAGACACAC-3' (SEQ ID NO:3); and

ACM14: 5'-CGCGGATCCTCCTCATGAGCACCCACAGCGGTC-3' (SEQ ID NO:4)

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PCR using these primers was carried out with one μ g human genomic DNA at 94°C for 1 min, 58°C for 2 min, and 72°C for 2 min for 30 cycles. The PCR product was digested with Bam HI, gel-purified, and subcloned in the Bluescript vector (Stratagene, San Francisco, CA).

5

EXAMPLE 2

EXPRESSION PATTERN AND SEQUENCE OF GDF-8

To determine the expression pattern of GDF-8, RNA samples prepared from a variety of adult tissues were screened by Northern analysis. RNA isolation and Northern analysis were carried out as described previously (Lee, S.J., *Mol. Endocrinol.*, 4:1034, 1990) except that hybridization was carried out in 5X SSPE, 10% dextran sulfate, 50%
10 formamide, 1% SDS, 200 μ g/ml salmon DNA, and 0.1% each of bovine serum albumin, ficoll, and polyvinylpyrrolidone. Five micrograms of twice poly A-selected RNA prepared from each tissue (except for muscle, for which only 2 μ g RNA was used) were electrophoresed on formaldehyde gels, blotted, and probed with GDF-8. As shown in
15 FIGURE 1, the GDF-8 probe detected a single mRNA species expressed at highest levels in muscle and at significantly lower levels in adipose tissue.

To obtain a larger segment of the GDF-8 gene, a mouse genomic library was screened with a probe derived from the GDF-8 PCR product. The partial sequence of a GDF-8 genomic clone is shown in FIGURE 2a. The sequence contains an open reading frame
20 corresponding to the predicted C-terminal region of the GDF-8 precursor protein. The predicted GDF-8 sequence contains two potential proteolytic processing sites, which are boxed. Cleavage of the precursor at the second of these sites would generate a mature C terminal fragment 109 amino acids in length with a predicted molecular weight of 12,400. The partial sequence of human GDF-8 is shown in FIGURE 2b. Assuming no
25 PCR-induced errors during the isolation of the human clone, the human and mouse amino acid sequences in this region are 100% identical.

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The C-terminal region of GDF-8 following the putative proteolytic processing site shows significant homology to the known members of the TGF- β superfamily (FIGURE 3). FIGURE 3 shows the alignment of the C-terminal sequences of GDF-8 with the corresponding regions of human GDF-1 (Lee, *Proc. Natl. Acad. Sci. USA*, 88:4250-4254, 1991), human BMP-2 and 4 (Wozney, *et al.*, *Science*, 242:1528-1534, 1988), human Vgr-1 (Celeste, *et al.* *Proc. Natl. Acad. Sci. USA*, 87:9843-9847, 1990), human OP-1 (Ozkaynak, *et al.*, *EMBO J.*, 9:2085-2093, 1990), human BMP-5 (Celeste, *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:9843-9847, 1990), human BMP-3 (Wozney, *et al.*, *Science*, 242:1528-1534, 1988), human MiS (Cate, *et al.* *Cell*, 45:685-698, 1986), human inhibin alpha, β A, and β B (Mason, *et al.*, *Biochem. Biophys. Res. Commun.*, 135:957-964, 1986), human TGF- β 1 (Derynck, *et al.*, *Nature*, 316:701-705, 1985), human TGF-R2 (deMartin, *et al.*, *EMBO J.*, 6:3673-3677, 1987), and human TGF- β 3 (ten Dijke, *et al.*, *Proc. Natl. Acad. Sci. USA*, 85:4715-4719, 1988). The conserved cysteine residues are boxed. Dashes denote gaps introduced in order to maximize the alignment.

GDF-8 contains most of the residues that are highly conserved in other family members, including the seven cysteine residues with their characteristic spacing. Like the TGF- β s and inhibin β s, GDF-8 also contains two additional cysteine residues. In the case of TGF- β 2, these two additional cysteine residues are known to form an intramolecular disulfide bond (Daopin, *et al.*, *Science*, 257:369, 1992; Schlunegger and Grutter, *Nature*, 358:430, 1992).

FIGURE 4 shows the amino acid homologies among the different members of the TGF- β superfamily. Numbers represent percent amino acid identities between each pair calculated from the first conserved cysteine to the C terminus. Boxes represent homologies among highly-related members within particular subgroups. In this region, GDF-8 is most homologous to Vgr-1 (45% sequence identity).

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EXAMPLE 3**ISOLATION OF cDNA CLONES ENCODING MURINE AND HUMAN GDF-8**

In order to isolate full-length cDNA clones encoding murine and human GDF-8, cDNA libraries were prepared in the lambda ZAP II vector (Stratagene) using RNA prepared from skeletal muscle. From 5 µg of twice poly A-selected RNA prepared from murine and human muscle, cDNA libraries consisting of 4.4 million and 1.9 million recombinant phage, respectively, were constructed according to the instructions provided by Stratagene. These libraries were screened without amplification. Library screening and characterization of cDNA inserts were carried out as described previously (Lee, *Mol. Endocrinol.*, 4:1034-1040).

From 2.4×10^6 recombinant phage screened from the murine muscle cDNA library, greater than 280 positive phage were identified using a murine GDF-8 probe derived from a genomic clone, as described in Example 1. The entire nucleotide sequence of the longest cDNA insert analyzed is shown in FIGURE 5a and 5b and SEQ ID NO:11. The 2676 base pair sequence contains a single long open reading frame beginning with a methionine codon at nucleotide 104 and extending to a TGA stop codon at nucleotide 1232. Upstream of the putative initiating methionine codon is an in-frame stop codon at nucleotide 23. The predicted pre-pro-GDF-8 protein is 76 amino acids in length. The sequence contains a core of hydrophobic amino acids at the N-terminus suggestive of a signal peptide for secretion (FIGURE 6a), one potential N-glycosylation site at asparagine 72, a putative RXXR proteolytic cleavage site at amino acids 264-267, and a C-terminal region showing significant homology to the known members of the TGF- β superfamily. Cleavage of the precursor protein at the putative RXXR site would generate a mature C-terminal GDF-8 fragment 109 amino acids in length with a predicted molecular weight of approximately 12,400.

From 1.9×10^6 recombinant phage screened from the human muscle cDNA library, 4 positive phage were identified using a human GDF-8 probe derived by polymerase chain reaction on human genomic DNA. The entire nucleotide sequence of the longest cDNA

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insert is shown in FIGURE 5c and 5d and SEQ ID NO:13. The 2743 base pair sequence contains a single long open reading frame beginning with a methionine codon at nucleotide 59 and extending to a TGA stop codon at nucleotide 1184. The predicted pre-pro-GDF-8 protein is 375 amino acids in length. The sequence contains a core of hydrophobic amino acids at the N-terminus suggestive of a signal peptide for secretion (FIGURE 6b), one potential N-glycosylation site at asparagine 71, and a putative RX(R proteolytic cleavage site at amino acids 263-266. FIGURE 7 shows a comparison of the predicted murine (top) and human (bottom) GDF-8 amino acid sequences. Numbers indicate amino acid position relative to the N-terminus. Identities between the two sequences are denoted by a vertical line. Murine and human GDF-8 are approximately 94% identical in the predicted pro-regions and 100% identical following the predicted RXXR cleavage sites.

EXAMPLE 4

DIMERIZATION OF GDF-8

To determine whether the processing signals in the GDF-8 sequence are functional and whether GDF-8 forms dimers like other members of the TGF- β superfamily, the GDF-8 cDNA was stably expressed in CHO cells. The GDF-8 coding sequence was cloned into the pMSXND expression vector (Lee and Nathans, *J. Biol. Chem.*, 263:3521,(1988) and transfected into CHO cells. Following G418 selection, the cells were selected in 0.2 μ M methotrexate, and conditioned medium from resistant cells was concentrated and electrophoresed on SDS gels. Conditioned medium was prepared by Cell Trends, Inc. (Middletown, MD). For preparation of anti-GDF-8 serum, the C-terminal region of GDF-8 (amino acids 268 to 376) was expressed in bacteria using the RSET vector (Invitrogen, San Diego, CA), purified using a nickle chelate column, and injected into rabbits. All immunizations were carried out by Spring Valley Labs (Woodbine, MD). Western analysis using [125 I]iodoprotein A was carried out as described (Burnette, W.N., *Anal. Biochem.*, 112:195, 1981). Western analysis of conditioned medium prepared from these cells using an antiserum raised against a bacterially-expressed C-terminal fragment of GDF-8 detected two protein species with apparent molecular weights of approximately

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52K and 15K under reducing conditions, consistent with unprocessed and processed forms of GDF-8, respectively. No bands were obtained either with preimmune serum or with conditioned medium from CHO cells transfected with an antisense construct. Under non-reducing conditions, the GDF-8 antiserum detected two predominant protein species with apparent molecular weights of approximately 101K and 25K, consistent with dimeric forms of unprocessed and processed GDF-8, respectively. Hence, like other TGF- β family members, GDF-8 appears to be secreted and proteolytically processed, and the C-terminal region appears to be capable of forming a disulfide-linked dimer.

EXAMPLE 5

PREPARATION OF ANTIBODIES AGAINST GDF-8 AND EXPRESSION OF GDF-8 IN MAMMALIAN CELLS

In order to prepare antibodies against GDF-8, GDF-8 antigen was expressed as a fusion protein in bacteria. A portion of murine GDF-8 cDNA spanning amino acids 268-376 (mature region) was inserted into the pRSET vector (Invitrogen) such that the GDF-8 coding sequence was placed in frame with the initiating methionine codon present in the vector; the resulting construct created an open reading frame encoding a fusion protein with a molecular weight of approximately 16,600. The fusion construct was transformed into BL21 (DE3) (pLysS) cells, and expression of the fusion protein was induced by treatment with isopropylthio- β -galactoside as described (Rosenberg, *et al.*, *Gene*, 56:125-135). The fusion protein was then purified by metal chelate chromatography according to the instructions provided by Invitrogen. A Coomassie blue-stained gel of unpurified and purified fusion proteins is shown in FIGURE 8.

The purified fusion protein was used to immunize both rabbits and chickens. Immunization of rabbits was carried out by Spring Valley Labs (Sykesville, MD), and immunization of chickens was carried out by HRP, Inc. (Denver, PA). Western analysis of sera both from immunized rabbits and from immunized chickens demonstrated the presence of antibodies directed against the fusion protein.

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To express GDF-8 in mammalian cells, the murine GDF-8 cDNA sequence from nucleotides 48-1303 was cloned in both orientations downstream of the metallothionein I promoter in the pMSXND expression vector; this vector contains processing signals derived from SV40, a dihydrofolate reductase gene, and a gene conferring resistance to the antibiotic G418 (Lee and Nathans, *J. Biol. Chem.*, 263:3521-3527). The resulting constructs were transfected into Chinese hamster ovary cells, and stable transfectants were selected in the presence of G418. Two milliliters of conditioned media prepared from the G418-resistant cells were dialyzed, lyophilized, electrophoresed under denaturing, reducing conditions, transferred to nitrocellulose, and incubated with anti-GDF-8 antibodies (described above) and [¹²⁵I]iodoproteinA.

As shown in FIGURE 9, the rabbit GDF-8 antibodies (at a 1:500 dilution) detected a protein of approximately the predicted molecular weight for the mature C-terminal fragment of GDF-8 in the conditioned media of cells transfected with a construct in which GDF-8 had been cloned in the correct (sense) orientation with respect to the metallothionein promoter (lane 2); this band was not detected in a similar sample prepared from cells transfected with a control antisense construct (lane 1). Similar results were obtained using antibodies prepared in chickens. Hence, GDF-8 is secreted and proteolytically processed by these transfected mammalian cells.

EXAMPLE 6

EXPRESSION PATTERN OF GDF-8

To determine the pattern of GDF-8, 5 µg of twice poly A-selected RNA prepared from a variety of murine tissue sources were subjected to Northern analysis. As shown in FIGURE 10a (and as shown previously in Example 2), the GDF-8 probe detected a single mRNA species present almost exclusively in skeletal muscle among a large number of adult tissues surveyed. On longer exposures of the same blot, significantly lower but detectable levels of GDF-8 mRNA were seen in fat, brain, thymus, heart, and lung. Hence, these results confirm the high degree of specificity of GDF-8 expression in skeletal muscle. GDF-8 mRNA was also detected in mouse embryos at both gestational

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ages (day 12.5 and day 18.5 post-coital) examined but not in placentas at various stages of development (FIGURE 10b).

To further analyze the expression pattern of GDF-8, *in situ* hybridization was performed on mouse embryos isolated at various stages of development.

- 5 For all *in situ* hybridization experiments, probes corresponding to the C-terminal region of GDF-8 were excluded in order to avoid possible cross-reactivity with other members of the superfamily. Whole mount *in situ* hybridization analysis was carried out as described (Wilkinson, D.G., *In Situ Hybridization, A Practical Approach*, pp. 75-83, IRL Press, Oxford, 1992) except that blocking and antibody incubation steps were
- 10 carried out as in Knecht *et al.* (Knecht, *et al.*, *Development*, 121:1927, 1995). Alkaline phosphatase reactions were carried out for 3 hours for day 10.5 embryos and overnight for day 9.5 embryos. Hybridization was carried out using digoxigenin- labelled probes spanning nucleotides 8-811 and 1298-2676, which correspond to the pro- region and 3' untranslated regions, respectively. *In situ* hybridization to sections was carried out as
- 15 described (Wilkinson, *et al.*, *Cell*, 50:79, 1987) using ³⁵S-labelled probes ranging from approximately 100-650 bases in length and spanning nucleotides 8-793 and 1566-2595. Following hybridization and washing, slides were dipped in NTB-3 photographic emulsion, exposed for 16-19 days, developed and stained with either hematoxylin and eosin or toluidine blue. RNA isolation, poly A selection, and Northern analysis were
- 20 carried out as described previously (McPherron and Lee, *J. Biol. Chem.*, 268:3444, 1993).

At all stages examined, the expression of GDF-8 mRNA appeared to be restricted to developing skeletal muscle. At early stages, GDF-8 expression was restricted to developing somites. By whole mount *in situ* hybridization analysis, GDF-8 mRNA could

25 first be detected as early as day 9.5 post coitum in approximately one-third of the somites. At this stage of development, hybridization appeared to be restricted to the most mature (9 out of 21 in this example), rostral somites. By day 10.5 p.c., GDF-8 expression was clearly evident in almost every somite (28 out of 33 in this example

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shown). Based on *in situ* hybridization analysis of sections prepared from day 10.5 p.c. embryos, the expression of GDF-8 in somites appeared to be localized to the myotome compartment. At later stages of development, GDF-8 expression was detected in a wide range of developing muscles.

- 5 GDF-8 continues to be expressed in adult animals as well. By Northern analysis, GDF-8 mRNA expression was seen almost exclusively in skeletal muscle among the different adult tissues examined. A significantly lower though clearly detectable signal was also seen in adipose tissue. Based on Northern analysis of RNA prepared from a large number of different adult skeletal muscles, GDF-8 expression appeared to be widespread
10 although the expression levels varied among individual muscles.

EXAMPLE 7

CHROMOSOMAL LOCALIZATION OF GDF-8

- In order to map the chromosomal location of GDF-8, DNA samples from human/rodent somatic cell hybrids (Drwinga, *et al.*, *Genomics*, 16:311-413, 1993; Dubois and Naylor,
15 *Genomics*, 16:315-319, 1993) were analyzed by polymerase chain reaction followed by Southern blotting. Polymerase chain reaction was carried out using primer #83, 5'-C-GCGGATCCGTGGATCTAAATGAGAACAGTGAGC-3' (SEQ ID NO: 15) and primer #84, 5'-CGCGAATTCTCAGGTAATGATTGTTCCGTTGTAGCG-3' (SEQ ID NO:16) for 40 cycles at 94°C for 2 minutes, 60°C for 1 minute, and 72°C for 2 minutes. These
20 primers correspond to nucleotides 119 to 143 (flanked by a Bam H1 recognition sequence), and nucleotides 394 to 418 (flanked by an Eco R1 recognition sequence), respectively, in the human GDF-8 cDNA sequence. PCR products were electrophoresed on agarose gels, blotted, and probed with oligonucleotide #100, 5'-ACACTAAATCTTCAAGAATA-3' (SEQ ID NO:17), which corresponds to a
25 sequence internal to the region flanked by primer #83 and #84. Filters were hybridized in 6 X SSC, 1 X Denhardt's solution, 100µg/ml yeast transfer RNA, and 0.05% sodium pyrophosphate at 50°C.

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As shown in FIGURE 11, the human-specific probe detected a band of the predicted size (approximately 320 base pairs) in the positive control sample (total human genomic DNA) and in a single DNA sample from the human/rodent hybrid panel. This positive signal corresponds to human chromosome 2. The human chromosome contained in each of the hybrid cell lines is identified at the top of each of the first 24 lanes (1-22, X, and Y). In the lanes designated M, CHO, and H, the starting DNA template was total genomic DNA from mouse, hamster, and human sources, respectively. In the lane marked B1, no template DNA was used. Numbers at left indicate the mobilities of DNA standards. These data show that the human GDF-8 gene is located on chromosome 2.

10

EXAMPLE 8

GDF-8 TRANSGENIC KNOCKOUT MICE

The GDF-8, we disrupted the GDF-8 gene was disrupted by homologous targeting in embryonic stem cells. To ensure that the resulting mice would be null for GDF-8 function, the entire mature C-terminal region was deleted and replaced by a neo cassette (Figure 12a). A murine 129 SV/J genomic library was prepared in lambda FIX II according to the instructions provided by Stratagene (La Jolla, CA). The structure of the GDF-8 gene was deduced from restriction mapping and partial sequencing of phage clones isolated from this library. Vectors for preparing the targeting construct were kindly provided by Philip Soriano and Kirk Thomas University. R1 ES cells were transfected with the targeting construct, selected with gancyclovir (2 μ M) and G418 (250 μ g/ml), and analyzed by Southern analysis. Homologously targeted clones were injected into C57BL/6 blastocysts and transferred into pseudopregnant females. Germline transmission of the targeted allele was obtained in a total of 9 male chimeras from 5 independently-derived ES clones. Genomic Southern blots were hybridized at 42°C as described above and washed in 0.2X SSC, 0.1% SDS at 42°C.

For whole leg analysis, legs of 14 week old mice were skinned, treated with 0.2 M EDTA in PBS at 4°C for 4 weeks followed by 0.5 M sucrose in PBS at 4°C. For fiber number and size analysis, samples were directly mounted and frozen in isopentane as described (Brumback and Leech, *Color Atlas of Muscle Histochemistry*, pp. 9-33, PSG Publishing

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Company, Littleton, MA, 1984). Ten to 30 μm sections were prepared using a cryostat and stained with hematoxylin and eosin. Muscle fiber numbers were determined from sections taken from the widest part of the tibialis cranialis muscle. Muscle fiber sizes were measured from photographs of sections of tibialis cranialis and gastrocnemius muscles. Fiber type analysis was carried out using the mysosin ATPase assay after pretreatment at pH 4.35 as described (Cumming, *et al.*, *Color Atlas of Muscle Pathology*, pp. 184-185, 1994) and by immunohistochemistry using an antibody directed against type I myosin (MY32, Sigma) and the Vectastain method (Vector Labs); in the immunohistochemical experiments, no staining was seen when the primary antibodies were left out. Carcasses were prepared from shaved mice by removing the all of the internal organs and associated fat and connective tissue. Fat content of carcasses from 4 month old males was determined as described (Leshner, *et al.*, *Physiol. Behavior*, 9:281, 1972).

For protein and DNA analysis, tissue was homogenized in 150 mM NaCl, 100 mM EDTA. Protein concentrations were determined using the Biorad protein assay. DNA was isolated by adding SDS to 1%, treating with 1 mg/ml proteinase K overnight at 55°C, extracting 3 times with phenol and twice with chloroform, and precipitating with ammonium acetate and EtOH. DNA was digested with 2 mg/ml RNase for 1 hour at 37°C, and following proteinase K digestion and phenol and chloroform extractions, the DNA was precipitated twice with ammonium acetate and EtOH.

Homologous targeting of the GDF-8 gene was seen in 13/131 gancyclovir/G418 doubly-resistant ES cell clones. Following injection of these targeted clones into blastocysts, we obtained chimeras from 5 independently-derived ES clones that produced heterozygous pups when crossed to C57BL/6 females (Figure 12b). Genotypic analysis of 678 offspring derived from crosses of F1 heterozygotes showed 170 +/- (25%), 380 +/- (56%), and 128 -/- (19%). Although the ratio of genotypes was close to the expected ratio of 1:2:1, the smaller than expected number of homozygous mutants appeared to be statistically significant ($p < 0.001$).

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Homozygous mutants were viable and fertile when crossed to C57BL/6 mice and to each other. Homozygous mutant animals, however, were approximately 30% larger than their heterozygous and wild type littermates (Table 1). The difference between mutant and wild type body weights appeared to be relatively constant irrespective of age and sex in
5 adult animals. Adult mutants also displayed an abnormal body shape, with pronounced shoulders and hips. When the skin was removed from animals that had been sacrificed, it was apparent that the muscles of the mutants were much larger than those of wild type animals. The increase in skeletal muscle mass appeared to be widespread throughout the body. Individual muscles isolated from homozygous mutant animals weighed
10 approximately 2-3 times more than those isolated from wild type littermates (Table 2). Although the magnitude of the weight increase appeared to roughly correlate with the level of GDF-8 expression in the muscles examined. To determine whether the increased muscle mass could account for the entire difference in total body weights between wild type and mutant animals or whether many tissues were generally larger in the mutants,
15 we compared the total body weights to carcass weights. As shown in Table 3, the difference in carcass weights between wild type and mutant animals was comparable to the difference in total body weights. Moreover, because the fat content of mutant and wild type animals was similar, these data are consistent with all of the total body weight difference resulting from an increase in skeletal muscle mass, although we have not
20 formally ruled out the possibility that differences in bone mass might also contribute to the differences in total body mass.

To determine whether the increase in skeletal muscle mass resulted from hyperplasia or from hypertrophy, histologic analysis of several different muscle groups was performed. The mutant muscle appeared grossly normal. No excess connective tissue or fat was seen
25 nor were there any obvious signs of degeneration, such as widely varying fiber sizes (see below) or centrally-placed nuclei. Quantitation of the number of muscle fibers showed that at the widest portion of the tibialis cranialis muscle, the total cell number was 86% higher in mutant animals compared to wild type littermates [mutant = 5470 +/- 121 (n = 3), wild type = 2936 +/- 288 (n = 3); $p < 0.01$]. Consistent with this result was the
30 finding that the amount of DNA extracted from mutant muscle was roughly 50% higher

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- than from wild type muscle [mutant = 350 μ g (n = 4), wild type = 233 μ g (n = 3) from pooled gastrocnemius, plantaris, triceps brachii, tibialis cranialis, and pectoralis muscles; p = 0.05]. Hence, a large part of the increase in skeletal muscle mass resulted from muscle cell hyperplasia. However, muscle fiber hypertrophy also appeared to contribute
- 5 to the overall increase in muscle mass. As shown in Figure 13, the mean fiber diameter of the tibialis cranialis muscle and gastrocnemius muscle was 7% and 22% larger, respectively, in mutant animals compared to wild type littermates, suggesting that the cross-sectional area of the fibers was increased by approximately 14% and 49%, respectively. Notably, although the mean fiber diameter was larger in the mutants, the
- 10 standard deviation in fiber sizes was similar between mutant and wild type muscle, consistent with the absence of muscle degeneration in mutant animals. The increase in fiber size was also consistent with the finding that the protein to DNA ratio (w/w) was slightly increased in mutant compared to wild type muscle [mutant = 871 +/- 111 (n = 4), wild type = 624 +/- 85 (n = 3); p < 0.05].
- 15 Table 4 shows a comparison between muscle weight (in grams) from wild-type (+/+), heterozygous (+/-) and a homozygous knock-out mice (-/-). The muscle mass is increased in heterozygous as compared to wild-type animals.

- Finally, fiber type analysis of various muscles was carried out to determine whether the number of both type I (slow) and type II (fast) fibers was increased in the mutant
- 20 animals. In most of the muscles examined, including the tibialis cranialis muscle, the vast majority of muscle fibers were type II in both mutant and wild type animals. Hence, based on the cell counts discussed above, the absolute number of type II fibers were increased in the tibialis cranialis muscle. In the soleus muscle, where the number of type I fibers was sufficiently high that we could attempt to quantitate the ratio of fiber types
- 25 could be quantiated, the percent of type I fibers was decreased by approximately 33% in mutant compared to wild type muscle [wild type = 39.2 +/- 8.1 (n = 3), mutant = 26.4 +/- 9.3 (n = 4)]; however, the variability in this ratio for both wild type and mutant animals was too high to support any firm conclusions regarding the relative number of fiber types.

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EXAMPLE 9
ISOLATION OF RAT AND CHICKEN GDF-8

- In order to isolate rat and chicken GDF-8 cDNA clones, skeletal muscle cDNA libraries prepared from these species were obtained from Stratagene and screened with a murine GDF-8 probe. Library screening was carried out as described previously (Lee, Mol. Endocrinol., 4:1034-1040) except that final washes were carried out in 2 X SSC at 65 °C. Partial sequence analysis of hybridizing clones revealed the presence of open reading frames highly related to murine and human GDF-8. Partial sequences of rat and chicken GDF-8 are shown in Figures 2c and 2d, respectively, and an alignment of the predicated rat and chicken GDF-8 amino acid sequences with those of murine and human GDF-8 are shown in Figure 3b. Full length rat and chicken GDF-8 is shown in Figures 14d and 14c, respectively and sequence alignment between murine, rat, human, baboon, porcine, ovine, bovine, chicken, and turkey sequences is shown in Figures 15a and 15b. All sequences contain an RSRR sequence that is likely to represent the proteolytic processing site. Following this RSRR sequence, the sequences contain a C-terminal region that is 100% conserved among all four species. The absolute conservation of the C-terminal region between species as evolutionarily far apart as humans and chickens, and baboons and turkeys, suggests that this region will be highly conserved in many other species as well.
- Similar methodology was used to obtain the nucleotide and amino acid sequences for baboon (SEQ ID NO:18 and 19, respectively; Figure 14a); bovine (SEQ ID NO:20 and 21, respectively; Figure 14b); turkey (SEQ ID NO:26 and 27, respectively; Figure 14e); porcine (SEQ ID NO:28 and 29, respectively; Figure 14f); and ovine (SEQ ID NO:30 and 31, respectively; Figure 14g).
- Although the invention has been described with reference to the presently preferred embodiment, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: The Johns Hopkins University School of Medicine
- (ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-8
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US98/-----
 - (B) FILING DATE: 05-February-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/795,071
 - (B) FILING DATE: 05-February-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/847,910
 - (B) FILING DATE: 28-April-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/862,445
 - (B) FILING DATE: 23-May-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lisa A. Haile, Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07265/129W01
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vii) IMMEDIATE SOURCE:

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(B) CLONE: SJL141

(ix) FEATURE:

(A) NAME/KEY: Modified Base

(B) LOCATION: 1...35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCG GNTGGVANRA YTGGRTNRTN NKCNC

35

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: SJL147

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1...33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCTC CANSRCARC TNTCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ACM13

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1...32

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCA GAAGTCAAGG TGACAGACAC AC

32

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(vii) IMMEDIATE SOURCE:
(B) CLONE: ACM14

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1...33
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCT CCTCATGAGC ACCACAGCG GTC

33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: mouse GDF-8

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 59...436
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTAAGGTAGG AAGGATTTC	GGCTCTATTT ACATAATTGT TCTTTCCTTT TCACACAG	58
AAT CCC TTT TTA GAA GTC AAG GTG ACA GAC ACA CCC AAG AGG TCC CGG		106
Asn Pro Phe Leu Glu Val Lys Val Thr Asp Thr Pro Lys Arg Ser Arg		
1 5 10 15		
AGA GAC TTT GGG CTT GAC TGC GAT GAG CAC TCC ACG GAA TCC CGG TGC		154
Arg Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr Glu Ser Arg Cys		
20 25 30		
TGC CGC TAC CCC CTC ACG GTC GAT TTT GAA GCC TTT GGA TGG GAC TGG		202
Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp Trp		
35 40 45		
ATT ATC GCA CCC AAA AGA TAT AAG GCC AAT TAC TGC TCA GGA GAG TGT		250
Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys		
50 55 60		
GAA TTT GTG TTT TTA CAA AAA TAT CCG CAT ACT CAT CTT GTG CAC CAA		298
Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His Gln		
65 70 75 80		
GCA AAC CCC AGA GGC TCA GCA GGC CCT TGC TGC ACT CCG ACA AAA ATG		346
Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys Met		
85 90 95		

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TCT CCC ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA TAT 394
 Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr
 100 105 110

GGG AAA ATT CCA GCC ATG GTA GTA GAC CGC TGT GGG TGC TCA TGAGCTTTGC 446
 Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
 115 120 125

ATTAGGTTAG AAACCTCCCA AGTCATGGAA GGTCTTCCCC TCAATTTCTGA AACTGTGAAT 506
 TCCTGCAGCC CGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACC 550

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg
1				5					10					15	
Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys
			20					25					30		
Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp
		35					40					45			
Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys
	50					55					60				
Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln
65				70					75					80	
Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met
			85					90						95	
Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr
			100					105					110		
Gly	Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser		
		115				120						125			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: human GDF-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3...326
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

- 59 -

CA AAA AGA TCC AGA AGG GAT TTT GGT CTT GAC TGT GAT GAG CAC TCA	47
Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His Ser	
1 5 10 15	
ACA GAA TCA CGA TGC TGT CGT TAC CCT CTA ACT GTG GAT TTT GAA GCT	95
Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala	
20 25 30	
TTT GGA TGG GAT TGG ATT ATC GCT CCT AAA AGA TAT AAG GCC AAT TAC	143
Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr	
35 40 45	
TGC TCT GGA GAG TGT GAA TTT GTA TTT TTA CAA AAA TAT CCT CAT ACT	191
Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr	
50 55 60	
CAT CTG GTA CAC CAA GCA AAC CCC AGA GGT TCA GCA GGC CCT TGC TGT	239
His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys	
65 70 75	
ACT CCC ACA AAG ATG TCT CCA ATT AAT ATG CTA TAT TTT AAT GGC AAA	287
Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys	
80 85 90 95	
GAA CAA ATA ATA TAT GGG AAA ATT CCA GCG ATG GTA GTA	326
Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val	
100 105	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His Ser Thr	
1 5 10 15	
Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe	
20 25 30	
Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys	
35 40 45	
Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His	
50 55 60	
Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr	
65 70 75 80	
Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Lys Glu	
85 90 95	
Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val	
100 105	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid

- 60 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL141

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1...9
(D) OTHER INFORMATION: "Xaa at position 3 = His, Gln, Asn, Lys, Asp, or Glu; Xaa at position 4 = Asp or Asn; Xaa at positions 6 and 7 is Val, Ile, or Met; Xaa at position 8 = Ala or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: SJL147

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1...8
(D) OTHER INFORMATION: "Xaa at position 2 = Val, Ile, Met, Thr or Ala; Xaa at position 4 = Asp or Glu; Xaa at position 7 = Gly, or Ala.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Xaa Val Xaa Ser Cys Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Murine GDF-8

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1...2676
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCTCTCGGA CGGTACATGC ACTAATATTT CACTTGGCAT TACTCAAAAG CAAAAGAAG

- 61 -

AAATAAGAAC AAGGGAAAAA AAAAGATTGT GCTGATTTTT AAA	ATG	ATG	CAA	AAA	115
	Met	Met	Gln	Lys	
	1				
CTG CAA ATG TAT GTT TAT ATT TAC CTG TTC ATG CTG ATT GCT GCT GGC					163
Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly					
5 10 15 20					
CCA GTG GAT CTA AAT GAG GGC AGT GAG AGA GAA GAA AAT GTG GAA AAA					211
Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys					
25 30 35					
GAG GGG CTG TGT AAT GCA TGT GCG TGG AGA CAA AAC ACG AGG TAC TCC					259
Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser					
40 45 50					
AGA ATA GAA GCC ATA AAA ATT CAA ATC CTC AGT AAG CTG CGC CTG GAA					307
Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu					
55 60 65					
ACA GCT CCT AAC ATC AGC AAA GAT GCT ATA AGA CAA CTT CTG CCA AGA					355
Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg					
70 75 80					
GCG CCT CCA CTC CGG GAA CTG ATC GAT CAG TAC GAC GTC CAG AGG GAT					403
Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp					
85 90 95 100					
GAC AGC AGT GAT GGC TCT TTG GAA GAT GAC GAT TAT CAC GCT ACC ACG					451
Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr His Ala Thr Thr					
105 110 115					
GAA ACA ATC ATT ACC ATG CCT ACA GAG TCT GAC TTT CTA ATG CAA GCG					499
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala					
120 125 130					
GAT GGC AAG CCC AAA TGT TGC TTT TTT AAA TTT AGC TCT AAA ATA CAG					547
Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln					
135 140 145					
TAC AAC AAA GTA GTA AAA GCC CAA CTG TGG ATA TAT CTC AGA CCC GTC					595
Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg Pro Val					
150 155 160					
AAG ACT CCT ACA ACA GTG TTT GTG CAA ATC CTG AGA CTC ATC AAA CCC					643
Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro					
165 170 175 180					
ATG AAA GAC GGT ACA AGG TAT ACT GGA ATC CGA TCT CTG AAA CTT GAC					691
Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys Leu Asp					
185 190 195					
ATG AGC CCA GGC ACT GGT ATT TGG CAG AGT ATT GAT GTG AAG ACA GTG					739
Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys Thr Val					
200 205 210					
TTG CAA AAT TGG CTC AAA CAG CCT GAA TCC AAC TTA GGC ATT GAA ATC					787
Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile					
215 220 225					
AAA GCT TTG GAT GAG AAT GGC CAT GAT CTT GCT GTA ACC TTC CCA GGA					835
Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr Phe Pro Gly					
230 235 240					

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CCA GGA GAA GAT GGG CTG AAT CCC TTT TTA GAA GTC AAG GTG ACA GAC Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp 245 250 255 260	883
ACA CCC AAG AGG TCC CGG AGA GAC TTT GGG CTT GAC TGC GAT GAG CAC Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His 265 270 275	931
TCC ACG GAA TCC CGG TGC TGC CGC TAC CCC CTC ACG GTC GAT TTT GAA Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu 280 285 290	979
GCC TTT GGA TGG GAC TGG ATT ATC GCA CCC AAA AGA TAT AAG GCC AAT Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn 295 300 305	1027
TAC TGC TCA GGA GAG TGT GAA TTT GTG TTT TTA CAA AAA TAT CCG CAT Tyr Cys Ser Gly Glu Cys Phe Val Phe Leu Gln Lys Tyr Pro His 310 315 320	1075
ACT CAT CTT GTG CAC CAA GCA AAC CCC AGA GGC TCA GCA GGC CCT TGC Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys 325 330 335 340	1123
TGC ACT CCG ACA AAA ATG TCT CCC ATT AAT ATG CTA TAT TTT AAT GGC Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly 345 350 355	1171
AAA GAA CAA ATA ATA TAT GGG AAA ATT CCA GCC ATG GTA GTA GAC CGC Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg 360 365 370	1219
TGT GGG TGC TCA TGAGCTTTGC ATTAGGTTAG AAACCTCCCA AGTCATGGAA GGTCT Cys Gly Cys Ser 375	1276
TCCCCTCAAT TTCGAAACTG TGAATTCAAG CACCACAGGC TGTAGGCCTT GAGTATGCTC	1336
TAGTAACGTA AGCACAAGCT ACAGTGTATG AACTAAAAGA GAGAATAGAT GCAATGGTTG	1396
GCATTCACCC ACCAAAATAA ACCATACTAT AGGATGTTGT ATGATTTCCA GAGTTTTTGA	1456
AATAGATGGA GATCAAATTA CATTTATGTC CATATATGTA TATTACAACT ACAATCTAGG	1516
CAAGGAAAGT AGAGCACATC TTGTGGTCTG CTGAGTTAGG AGGGTATGAT TAAAAGGTAA	1576
AGTCTTATTT CCTAACAGTT TCACCTAATA TTTACAGAAG AATCTATATG TAGCCTTTGT	1636
AAAGTGTAGG ATTGTTATCA TTTAAAAACA TCATGTACAC TTATATTTGT ATTGTATACT	1696
TGGTAAGATA AAATTCACCA AAGTAGGAAT GGGGCCTCAC ATACACATTG CCATTCCTAT	1756
TATAATTGGA CAATCCACCA CGGTGCTAAT GCAGTGTGTA ATGGCTCCTA CTGGACCTCT	1816
CGATAGAACA CTCTACAAAG TACGAGTCTC TCTCTCCCTT CCAGGTGCAT CTCCACACAC	1876
ACAGCACTAA GTGTTCAATG CATTTTCTTT AAGGAAAGAA GAATCTTTTT TTCTAGAGGT	1936
CACTTTTCAG TCAACTCTAG CACAGCGGGA GTGACTGCTG CATCTTAAAA GGCAGCCAAA	1996
CAGTATTCAT TTTTAAATCT AAATTTCAAA ATCACTGTCT GCCTTIATCA CATGGCAATT	2056
TTGTGGTAAA ATAATGGAAA TGAAGTGGTT TATCAATATT GTATAAAAGA CTCTGAAACA	2116
ATTACATTTA TATAATATGT ATACAATATT GTTTTGTAAG TAAGTGTCTC CTTTTATATT	2176
TACTTTGGTA TATTTTTTACA CTAATGAAAT TTCAAATCAT TAAAGTACAA AGACATGTCA	2236
TGTATCACAA AAAAGGTGAC TGCTTCTATT TCAGAGTGAA TTAGCAGATT CAATAGTGGT	2296
CTTAAACTC TGTATGTTAA GATTAGAAGG TTATATTACA ATCAATTTAT GTATTTTTTA	2356
CATTATCAAC TTATGGTTTC ATGGTGGCTG TATCTATGAA TGTGGCTCCC AGTCAAATTT	2416
CAATGCCCCA CCATTTTAAA AATTACAAGC ATTACTAAAC ATACCAACAT GTATCTAAAG	2476
AAATACAAAT ATGGTATCTC AATAACAGCT ACTTTTTTAT TTTATAATTT GACAATGAAT	2536
ACATTTCTTT TATTTACTTC AGTTTATATA ATTGGAACCT TGTATATCAA ATGTATTGTA	2596
CTCATAGCTA AATGAAATTA TTTCTTACAT AAAAATGTGT AGAAACTATA AATTAAAGTG	2656
TTTTACACATT TTTGAAAGGC	2676

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Met	Gln	Lys	Leu	Gln	Met	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu
1				5					10					15	
Ile	Ala	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Gly	Ser	Glu	Arg	Glu	Glu
			20					25					30		
Asn	Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn
		35				40					45				
Thr	Arg	Tyr	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys
	50				55						60				
Leu	Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln
65				70					75					80	
Leu	Leu	Pro	Arg	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp
			85					90					95		
Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr
		100						105				110			
His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe
	115					120						125			
Leu	Met	Gln	Ala	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser
130					135						140				
Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr
145				150					155					160	
Leu	Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg
			165					170					175		
Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser
	180						185					190			
Leu	Lys	Leu	Asp	Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp
	195					200						205			
Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu
	210				215						220				
Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val
225				230					235					240	
Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val
		245						250					255		
Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp
	260							265				270			
Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr
	275					280						285			
Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg
	290				295						300				
Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln
305				310					315					320	
Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser
		325						330					335		
Ala	Gly	Pro	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	
		340				345						350			
Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met
	355				360							365			
Val	Val	Asp	Arg	Cys	Gly	Cys	Ser								
370					375										

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2743 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Human GDF-8

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1...2743
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGAAAAGTA AAAGGAAGAA ACAAGAACAA GAAAAAAGAT TATATTGATT TTAAAATC	58
ATG CAA AAA CTG CAA CTC TGT GTT TAT ATT TAC CTG TTT ATG CTG ATT Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile 1 5 10 15	106
GTT GCT GGT CCA GTG GAT CTA AAT GAG AAC AGT GAG CAA AAA GAA AAT Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn 20 25 30	154
GTG GAA AAA GAG GGG CTG TGT AAT GCA TGT ACT TGG AGA CAA AAC ACT Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr 35 40 45	202
AAA TCT TCA AGA ATA GAA GCC ATT AAG ATA CAA ATC CTC AGT AAA CTT Lys Ser Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu 50 55 60	250
CGT CTG GAA ACA GCT CCT AAC ATC AGC AAA GAT GTT ATA AGA CAA CTT Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu 65 70 75 80	298
TTA CCC AAA GCT CCT CCA CTC CGG GAA CTG ATT GAT CAG TAT GAT GTC Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val 85 90 95	346
CAG AGG GAT GAC AGC AGC GAT GGC TCT TTG GAA GAT GAC GAT TAT CAC Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His 100 105 110	394
GCT ACA ACG GAA ACA ATC ATT ACC ATG CCT ACA GAG TCT GAT TTT CTA Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu 115 120 125	442
ATG CAA GTG GAT GGA AAA CCC AAA TGT TGC TTC TTT AAA TTT AGC TCT Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser 130 135 140	490
AAA ATA CAA TAC AAT AAA GTA GTA AAG GCC CAA CTA TGG ATA TAT TTG Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu 145 150 155 160	538
AGA CCC GTC GAG ACT CCT ACA ACA GTG TTT GTG CAA ATC CTG AGA CTC Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu 165 170 175	586
ATC AAA CCT ATG AAA GAC GGT ACA AGG TAT ACT GGA ATC CGA TCT CTG Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu 180 185 190	634

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AAA CTT GAC ATG AAC CCA GGC ACT GGT ATT TGG CAG AGC ATT GAT GTG Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val 195 200 205	682
AAG ACA GTG TTG CAA AAT TGG CTC AAA CAA CCT GAA TCC AAC TTA GGC Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly 210 215 220	730
ATT GAA ATA AAA GCT TTA GAT GAG AAT GGT CAT GAT CTT GCT GTA ACC Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr 225 230 235 240	778
TTC CCA GGA CCA GGA GAA GAT GGG CTG AAT CCG TTT TTA GAG GTC AAG Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys 245 250 255	826
GTA ACA GAC ACA CCA AAA AGA TCC AGA AGG GAT TTT GGT CTT GAC TGT Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys 260 265 270	874
GAT GAG CAC TCA ACA GAA TCA CGA TGC TGT CGT TAC CCT CTA ACT GTG Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val 275 280 285	922
GAT TTT GAA GCT TTT GGA TGG GAT TGG ATT ATC GCT CCT AAA AGA TAT Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr 290 295 300	970
AAG GCC AAT TAC TGC TCT GGA GAG TGT GAA TTT GTA TTT TTA CAA AAA Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys 305 310 315 320	1018
TAT CCT CAT ACT CAT CTG GTA CAC CAA GCA AAC CCC AGA GGT TCA GCA Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala 325 330 335	1066
GGC CCT TGC TGT ACT CCC ACA AAG ATG TCT CCA ATT AAT ATG CTA TAT Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr 340 345 350	1114
TTT AAT GGC AAA GAA CAA ATA ATA TAT GGG AAA ATT CCA GCG ATG GTA Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val 355 360 365	1162
GTA GAC CGC TGT GGG TGC TCA TGAGATTTAT ATTAAGCGTT CATAACTTCC TAAAAC Val Asp Arg Cys Gly Cys Ser 370 375	1219
ATGGAAGGTT TTCCCCTCAA CAATTTTGAA GCTGTGAAAT TAAGTACCAC AGGCTATAGG CCTAGAGTAT GCTACAGTCA CTTAAGCATA AGCTACAGTA TGTAAGCTAA AAGGGGGAAT ATATGCAATG GTTGGCATT T AACCATCCAA ACAAATCATA CAAGAAAGTT TTATGATTTC CAGAGTTTTT GAGCTAGAAG GAGATCAAAT TACATTTATG TTCCTATATA TTACAACATC GGCGAGGAAA TGAAAGCGAT TCTCCTTGAG TTCTGATGAA TTAAAGGAGT ATGCTTTAAA GTCTATTTCT TTAAAGTTTT GTTTAATATT TACAGAAAAA TCCACATACA GTATTGGTAA AATGCAGGAT TGTATATAC CATCATTCGA ATCATCCTTA AACACTTGAA TTTATATTGT ATGGTAGAT ACTTGGTAAG ATAAAATTCC ACAAAAATAG GGATGGTGCA GCATATGCAA TTTCCATTCC TATTATAATT GACACAGTAC ATTAACAATC CATGCCAACG GTGCTAATAC GATAGGCTGA ATGTCTGAGG CTACCAGGTT TATCACATAA AAAACATTCA GTAAAATAGT AAGTTTCTCT TTCTTTCAGG TGCATTTTCC TACACCTCCA AATGAGGAAT GGATTTTCTT TAATGTAAGA AGAATCAITT TTCTAGAGGT TGGCTTTCAA TTCTGTAGCA TACTGGAGA AACTGCATTA TCTTAAAAGG CAGTCAAATG GTGTTTGT TTATCAAAAT GTCAAAATAA CATACTTGA GAAGTATGTA ATTTTGTCTT TGGAAAAATTA CAACACTGCC TTTGCAACAC TGCAGTTTTT ATGGTAAAAT AATAGAAATG ATCGACTCTA TCAATATTGT ATAAAAAGAC TGAAACAATG CATTTATATA ATATGTATAC AATATTGTTT TGTAATAAG TGTCTCCTTT	1279 1339 1399 1459 1519 1579 1639 1699 1759 1819 1879 1939 1999 2059 2119 2179

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TTTATTTACT	TTGGTATATT	TTTACACTAA	GGACATTTCA	AATTAAGTAC	TAAGGCACAA	2239
AGACATGTCA	TGCATCACAG	AAAAGCAACT	ACTTATATTT	CAGAGCAAAT	TAGCAGATTA	2299
AATAGTGGTC	TTAAAACTCC	ATATGTTAAT	GATTAGATGG	TTATATTACA	ATCATTTTAT	2359
ATTTTITTTAC	ATGATTAACA	TTCACTTATG	GATTCATGAT	GGCTGTATAA	AGTGAATTTG	2419
AAATTTCAAT	GGTTTACTGT	CATTGTGTTT	AAATCTCAAC	GTTCCATTAT	TTTAATACTT	2479
GCAAAAACAT	TACTAAGTAT	ACCAAAATAA	TTGACTCTAT	TATCTGAAAT	GAAGAATAAA	2539
CTGATGCTAT	CTCAACAATA	ACTGTTACTT	TTATTTTATA	ATTTGATAAT	GAATATATTT	2599
CTGCATTTAT	TTACTTCTGT	TTTGTAATT	GGGATTTTGT	TAATCAAATT	TATTGTACTA	2659
TGACTAAATG	AAATTATTTT	TTACATCTAA	TTGTAGAAA	CAGTATAAGT	TATATTAAAG	2719
TGTTTTTACA	TTTTTTTGAA	AGAC				2743

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gln	Lys	Leu	Gln	Leu	Cys	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile
1				5					10					15	
Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn
			20					25					30		
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr
		35					40					45			
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu
	50					55					60				
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Val	Ile	Arg	Gln	Leu
65					70				75						
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val
			85					90					95		
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
			100					105					110		
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu
			115				120					125			
Met	Gln	Val	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser
	130					135					140				
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
145					150				155						160
Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu
			165					170						175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
		180						185					190		
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val
	195						200					205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
	210					215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
225					230				235						240
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
			245					250						255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
		260						265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
	275						280					285			
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290					295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
305					310					315					320

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Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
		355					360					365			
Val	Asp	Arg	Cys	Gly	Cys	Ser									
	370					375									

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: #83

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..34
(C) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGGATCCG TGGATCTAAA TGAGAACAGT GAGC

34

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: #84

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1...37
(C) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGAATTCT CAGGTAATGA TTGTTTCCGT TGTAGCG

37

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: #100

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1...20
(C) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
ACACTAAATC TTCAAGAATA 20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1055 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Baboon GDF-8

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1...1055
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

	ATG CAA AAA	9
	Met Gln Lys	
	1	
CTG CAA CTC TGT GTT TAT ATT TAC CTG TTT ATG CTG ATT GTT GCT GGT	54	
Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile Val Ala Gly		
5 10 15 20		
CCA GTG GAT CTA AAT GAG AAC AGT GAG CAA AAA GAA AAT GTG GAA AAA	95	
Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn Val Glu Lys		
25 30 35		
GAG GGG CTG TGT AAT GCA TGT ACT TGG AGA CAA AAC ACT AAA TCT TCA	140	
Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr Lys Ser Ser		
40 45 50		
AGA ATA GAA GCC ATT AAA ATA CAA ATC CTC AGT AAA CTT CGT CTG GAA	185	
Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu		
55 60 65		
ACA GCT CCT AAC ATC AGC AAA GAT GCT ATA AGA CAA CTT TTA CCC AAA	230	
Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Lys		
70 75 80		
GCG CCT CCA CTC CGG GAA CTG ATT GAT CAG TAT GAT GTC CAG AGG GAT	275	
Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp		
85 90 95 100		

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GAC Asp	AGC Ser	AGC Ser	GAT Asp	GGC Gly 105	TCT Ser	TTG Leu	GAA Glu	GAT Asp	GAC Asp 110	GAT Asp	TAT Tyr	CAC His	GCT Ala	ACA Thr 115	ACG Thr	320
GAA Glu	ACA Thr	ATC Ile	ATT Ile 120	ACC Thr	ATG Met	CCT Pro	ACA Thr	GAG Glu 125	TCT Ser	GAT Asp	TTT Phe	TTA Leu	ATG Met 130	CAA Gln	GTG Val	365
GAT Asp	GGA Gly	AAA Lys 135	CCC Pro	AAA Lys	TGT Cys	TGC Cys	TTC Phe 140	TTT Phe	AAA Lys	TTT Phe	AGC Ser	TCT Ser 145	AAA Lys	ATA Ile	CAA Gln	410
TAC Tyr 150	AAT Asn	AAA Lys	GTG Val	GTA Val	AAG Lys	GCC Ala 155	CAA Gln	CTA Leu	TGG Trp	ATA Ile	TAT Tyr 160	TTG Leu	AGA Arg	CCC Pro	GTC Val	455
GAG Glu 165	ACT Thr	CCT Pro	ACA Thr	ACA Thr	GTG Val 170	TTT Phe	GTG Val	CAA Gln	ATC Ile	CTG Leu 175	AGA Arg	CTC Leu	ATC Ile	AAA Lys	CCT Pro 180	500
ATG Met	AAA Lys	GAC Asp	GGT Gly	ACA Thr 185	AGG Arg	TAT Tyr	ACT Thr	GGA Gly	ATC Ile 190	CGA Arg	TCT Ser	CTG Leu	AAA Lys	CTT Leu	GAC Asp 195	545
ATG Met	AAC Ser	CCA Pro	GGC Gly 200	ACT Thr	GGT Gly	ATT Ile	TGG Trp	CAG Gln 205	AGC Ser	ATT Ile	GAT Asp	GTG Val	AAG Lys 210	ACA Thr	GTG Val	590
TTG Leu	CAA Gln 215	AAT Asn	TGG Trp	CTC Leu	AAA Lys	CAA Gln 220	CCT Pro	GAA Glu	TCC Ser	AAC Asn	TTA Leu	GGC Gly 225	ATT Ile	GAA Glu	ATA Ile	635
AAA Lys 230	GCT Ala	TTA Leu	GAT Asp	GAG Glu	AAT Asn 235	GGT Gly	CAT His	GAT Asp	CTT Leu	GCT Ala	GTA Val 240	ACC Thr	TTC Phe	CCA Pro	GGA Gly	680
CCA Pro 245	GGA Gly	GAA Glu	GAT Asp	GGG Gly 250	CTG Leu	AAT Asn	CCC Pro	TTT Phe	TTA Leu	GAG Glu 255	GTC Val	AAG Lys	GTA Val	ACA Thr	GAC Asp 260	725
ACA Thr	CCC Pro	AAA Lys	AGA Arg	TCC Ser 265	AGA Arg	AGG Arg	GAT Asp	TTT Phe 270	GGT Gly	CTT Leu	GAC Asp	TGT Cys	GAT Asp	GAG Glu 275	CAC His	770
TCA Ser	ACA Thr	GAA Glu	TCG Ser 280	CGA Arg	TGC Cys	TGT Cys	CGT Arg	TAC Tyr 285	CCT Pro	CTA Leu	ACT Thr	GTG Val	GAT Asp 290	TTT Phe	GAA Glu	815
GCT Ala	CTT Phe	GGA Gly 295	TGG Trp	GAT Asp	TGG Trp	ATT Ile	ATC Ile 300	GCT Ala	CCT Pro	AAA Lys	AGA Arg	TAT Tyr 305	AAG Lys	GCC Ala	AAT Asn	860
TAC Tyr 310	TGC Cys	TCT Ser	GGA Gly	GAG Glu	TGT Cys	GAA Glu 315	TTT Phe	GTA Val	TTT Phe	TTA Leu	CAA Gln 320	AAA Lys	TAT Tyr	CCT Pro	CAT His	905
ACT Thr 325	CAT His	CTG Leu	GTA Val	CAC His	CAA Gln 330	GCA Ala	AAC Asn	CCC Pro	AGA Arg	GGT Gly 335	TCA Ser	GCA Ala	GGC Gly	CCT Pro 340	TGC Cys	950
TGT Cys	ACT Thr	CCC Pro	ACA Thr 345	AAG Lys	ATG Met	TCT Ser	CCA Pro	ATT Ile 350	AAT Asn	ATG Met	CTA Leu	TAT Tyr	TTT Phe	AAT Asn 355	GGC Gly	995

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[illegible]

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: Baboon GDF-8

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1...376

(D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

														Met 1	Gln	Lys
Leu 5	Gln	Leu	Cys	Val	Tyr 10	Ile	Tyr	Leu	Phe	Met 15	Leu	Ile	Val	Ala	Gly 20	
Pro	Val	Asp	Leu	Asn 25	Glu	Asn	Ser	Glu	Gln 30	Lys	Glu	Asn	Val	Glu 35	Lys	
Glu	Gly	Leu	Cys 40	Asn	Ala	Cys	Thr	Trp 45	Arg	Gln	Asn	Thr	Lys 50	Ser	Ser	
Arg	Ile	Glu 55	Ala	Ile	Lys	Ile	Gln 60	Ile	Leu	Ser	Lys	Leu 65	Arg	Leu	Glu	
Thr	Ala 70	Pro	Asn	Ile	Ser	Lys 75	Asp	Ala	Ile	Arg	Gln 80	Leu	Leu	Pro	Lys	
Ala 85	Pro	Pro	Leu	Arg	Glu 90	Leu	Ile	Asp	Gln 95	Tyr	Asp	Val	Gln	Arg	Asp 100	
Asp	Ser	Ser	Asp 105	Gly	Ser	Leu	Glu	Asp 110	Asp	Asp	Tyr	His	Ala 115	Thr	Thr	
Glu	Thr	Ile 120	Ile	Thr	Met	Pro	Thr	Glu 125	Ser	Asp	Phe	Leu 130	Met	Gln	Val	
Asp	Gly	Lys 135	Pro	Lys	Cys	Cys	Phe 140	Phe	Lys	Phe	Ser	Ser 145	Lys	Ile	Gln	
Tyr	Asn 150	Lys	Val	Val	Lys	Ala 155	Gln	Leu	Trp	Ile	Tyr 160	Leu	Arg	Pro	Val	
Glu 165	Thr	Pro	Thr	Thr 170	Val	Phe	Val	Gln	Ile	Leu 175	Arg	Leu	Ile	Lys	Pro 180	
Met	Lys	Asp	Gly 185	Thr	Arg	Tyr	Thr	Gly 190	Ile	Arg	Ser	Leu 195	Lys	Leu	Asp	
Met	Ser	Pro 200	Gly	Thr	Gly	Ile	Trp 205	Gln	Ser	Ile	Asp	Val 210	Lys	Thr	Val	
Leu	Gln 215	Asn	Trp	Leu	Lys	Gln 220	Pro	Glu	Ser	Asn	Leu 225	Gly	Ile	Glu	Ile	
Lys	Ala 230	Leu	Asp	Glu	Asn 235	Gly	His	Asp	Leu	Ala 240	Val	Thr	Phe	Pro	Gly	
Pro 245	Gly	Glu	Asp	Gly 250	Leu	Asn	Pro	Phe	Leu	Glu 255	Val	Lys	Val	Thr	Asp 260	
Thr	Pro	Lys	Arg	Ser 265	Arg	Arg	Asp	Phe 270	Gly	Leu	Asp	Cys 275	Asp	Glu	His	
Ser	Thr	Glu 280	Ser	Arg	Cys	Cys	Arg 285	Tyr	Pro	Leu	Thr	Val 290	Asp	Phe	Glu	

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[illegible]

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Bovine GDF-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1...1055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

															ATG	CAA	AAA	9
															Met	Gln	Lys	
															1			
CTG	CAA	ATC	TCT	GTT	TAT	ATT	TAC	CTA	TTT	ATG	CTG	ATT	GTT	GCT	GGC	54		
Leu	Gln	Ile	Ser	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile	Val	Ala	Gly			
5					10					15					20			
CCA	GTG	GAT	CTG	AAT	GAG	AAC	AGC	GAG	CAG	AAG	GAA	AAT	GTG	GAA	AAA	95		
Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	Val	Glu	Lys			
				25					30					35				
GAG	GGG	CTG	TGT	AAT	GCA	TGT	TTG	TGG	AGG	GAA	AAC	ACT	ACA	TCG	TCA	140		
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Glu	Asn	Thr	Thr	Ser	Ser			
			40					45					50					
AGA	CTA	GAA	GCC	ATA	AAA	ATC	CAA	ATC	CTC	AGT	AAA	CTT	CGC	CTG	GAA	185		
Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu			
		55					60					65						
ACA	GCT	CCT	AAC	ATC	AGC	AAA	GAT	GCT	ATC	AGA	CAA	CTT	TTG	CCC	AAG	230		
Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Lys			
	70					75					80							
GCT	CCT	CCA	CTC	CTG	GAA	CTG	ATT	GAT	CAG	TTC	GAT	GTC	CAG	AGA	GAT	275		
Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val	Gln	Arg	Asp			
85					90					95					100			
GCC	AGC	AGT	GAC	GGC	TCC	TTG	GAA	GAC	GAT	GAC	TAC	CAC	GCC	AGG	ACG	320		
Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Arg	Thr			
				105					110					115				

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GAA	ACG	GTC	ATT	ACC	ATG	CCC	ACG	GAG	TCT	GAT	CTT	CTA	ACG	CAA	GTG	365
Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	Thr	Gln	Val	
			120					125					130			
GAA	GGA	AAA	CCC	AAA	TGT	TGC	TTC	TTT	AAA	TTT	AGC	TCT	AAG	ATA	CAA	410
Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln	
		135					140					145				
TAC	AAT	AAA	CTA	GTA	AAG	GCC	CAA	CTG	TGG	ATA	TAT	CTG	AGG	CCT	GTC	455
Tyr	Asn	Lys	Leu	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val	
	150					155					160					
AAG	ACT	CCT	GCG	ACA	GTG	TTT	GTG	CAA	ATC	CTG	AGA	CTC	ATC	AAA	CCC	500
Glu	Thr	Pro	Thr	Ala	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro	
165					170					175					180	
ATG	AAA	GAC	GGT	ACA	AGG	TAT	ACT	GGA	ATC	CGA	TCT	CTG	AAA	CTT	GAC	545
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp	
			185					190						195		
ATG	AAC	CCA	GGC	ACT	GGT	ATT	TGG	CAG	AGC	ATT	GAT	GTG	AAG	ACA	GTG	590
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val	
		200						205					210			
TTG	CAG	AAC	TGG	CTC	AAA	CAA	CCT	GAA	TCC	AAC	TTA	GGC	ATT	GAA	ATC	635
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile	
		215					220					225				
AAA	GCT	TTA	GAT	GAG	AAT	GGC	CAT	GAT	CTT	GCT	GTA	ACC	TTC	CCA	GAA	680
Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	Phe	Pro	Glu	
	230					235					240					
CCA	GGA	GAA	GAT	GGA	CTG	ACT	CCC	TTT	TTA	GAA	GTC	AAG	GTA	ACA	GAC	725
Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	
245					250					255					260	
ACA	CCA	AAA	AGA	TCT	AGG	AGA	GAT	TTT	GGG	CTT	GAT	TGT	GAT	GAA	CAC	770
Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His	
				265				270						275		
TCC	ACA	GAA	TCT	CGA	TGC	TGT	CGT	TAC	CCT	CTA	ACT	GTG	GAT	TTT	GAA	815
Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	
			280					285					290			
GCT	TTT	GGA	TGG	GAT	TGG	ATT	ATT	GCA	CCT	AAA	AGA	TAT	AAG	GCC	AAT	860
Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	
		295				300						305				
TAC	TGC	TCT	GGA	GAA	TGT	GAA	TTT	GTA	TTT	TTG	CAA	AAG	TAT	CCT	CAT	905
Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His	
	310					315					320					
ACC	CAT	CTT	GTG	CAC	CAA	GCA	AAC	CCC	AGA	GGT	TCA	GCC	GGC	CCC	TGC	950
Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys	
325					330					335					340	
TGT	ACT	CCT	ACA	AAG	ATG	TCT	CCA	ATT	AAT	ATG	CTA	TAT	TTT	AAT	GGC	995
Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Gly	
				345				350						355		
GAA	GGA	CAA	ATA	ATA	TAC	GGG	AAG	ATT	CCA	GCC	ATG	GTA	GTA	GAT	CGC	1040
Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	Val	Asp	Arg	
			360					365					370			

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TGT GGG TGT TCA TGA
Cys Gly Cys Ser
375

1055

(2) INFORMATION FOR SEO ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:21:

												Met	Gln	Lys	
												1			
Leu	Gln	Ile	Ser	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile	Val	Ala	Gly
5					10					15					20
Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	Val	Glu	Lys
				25					30						
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Glu	Asn	Thr	Thr	Ser	Ser
			40					45					50		
Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu
		55					60					65			
Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Lys
	70					75					80				
Ala	Pro	Pro	Leu	Leu	Glu	Leu	Ile	Asp	Gln	Phe	Asp	Val	Gln	Arg	Asp
85					90					95					100
Ala	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Arg	Thr
				105					110					115	
Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	Thr	Gln	Val
			120					125					130		
Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln
		135					140					145			
Tyr	Asn	Lys	Leu	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val
	150					155					160				
Glu	Thr	Pro	Thr	Ala	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro
165					170					175					180
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp
				185					190					195	
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val
			200					205					21		
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile
		215					220					225			
Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	Phe	Pro	Glu
	230					235					240				
Pro	Gly	Glu	Asp	Gly	Leu	Thr	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp
245					250					255					260
Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His
				265					270					275	
Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu
			280					285					290		
Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn
		295					300					305			
Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His
	310					315					320				
Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys

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Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg
360
Cys Gly Cys Ser
375

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1055 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: Chicken GDF-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1...1055

(D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22;

														ATG Met 1	CAA Gln	AAG Lys	9
CTG Leu 5	GCA Ala	GTC Val	TAT Tyr	GTT Val 10	TAT Tyr 10	ATT Ile	TAC Tyr	CTG Leu	TTC Phe	ATG Met 15	CAG Gln	ATC Ile	GCG Ala	GTT Val	GAT Asp 20	54	
CCG Pro	GTG Val	GCT Ala	CTG Leu	GAT Asp 25	GGC Gly	AGT Ser	AGT Ser	CAG Glu	CCC Gln 30	ACA Lys	GAG Glu	AAC Asn	GCT Val	GAA Glu 35	AAA Lys	95	
GAC Glu	GGA Gly	CTG Leu	TGC Cys 40	AAT Asn	GCT Ala	TGT Cys	ACG Thr	TGG Trp 45	AGA Arg	CAG Gln	AAT Asn	ACA Thr	AAA Lys 50	TCC Ser	TCC Ser	140	
AGA Arg	ATA Ile 55	GAA Glu 55	GCC Ala	ATA Ile	AAA Lys	ATT Ile	CAA Gln 60	ATC Ile	CTC Leu	AGC Ser	AAA Lys	CTG Leu 65	CGC Arg	CTG Leu	GAA Glu	185	
CAA Gln 70	GCA Ala 70	CCT Pro	AAC Asn	ATT Ile	AGC Ser	AGG Arg 75	GAC Asp 75	GTT Val	ATT Ile	AAG Lys	CAG Gln 80	CTT Leu	TTA Leu	CCC Pro	AAA Lys	230	
GCT Ala 85	CCT Pro	CCA Pro	CTG Leu	CAG Gln 90	GAA Glu 90	CTG Leu	ATT Ile	GAT Asp	CAG Gln	TAT Tyr 95	GAT Asp	GTC Val	CAG Gln	AGG Arg	GAC Asp 100	275	
GAC Asp	AGT Ser	AGC Ser	GAT Asp	GGC Gly 105	TCT Ser	TTG Leu	GAA Glu	GAC Asp	GAT Asp 110	GAC Asp	TAT Tyr	CAT His	GCC Ala	ACA Thr 115	ACC Thr	320	
GAG Glu	ACG Thr	ATT Ile	ATC Ile 120	ACA Thr	ATG Met	CCT Pro	ACG Thr	GAG Glu 125	TCT Ser	GAT Asp	TTT Phe	CTT Leu	GTA Val 130	CAA Gln	ATG Met	365	
GAG Glu	GGA Gly	AAA Lys 135	CCA Pro	AAA Lys	TGT Cys	TGC Cys	TTC Phe 140	TTT Phe	AAG Lys	TTT Phe	AGC Ser	TCT Ser 145	AAA Lys	ATA Ile	CAA Gln	410	

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TAT Tyr	AAC Asn	AAA Lys	GTA Val	GTA Val	AAG Lys	GCA Ala	CAA Gln	TTA Leu	TGG Trp	ATA Ile	TAC Tyr	TTG Leu	AGG Arg	CAA Gln	GTC Val	455
150						155					160					
CAA Gln	AAA Lys	CCT Pro	ACA Thr	ACG Thr	GTG Val	TTT Phe	GTG Val	CAG Gln	ATC Ile	CTG Leu	AGA Arg	CTC Leu	ATT Ile	AAG Lys	CCC Pro	500
165					170					175					180	
ATG Met	AAA Lys	GAC Asp	GGT Gly	ACA Thr	AGA Arg	TAT Tyr	ACT Thr	GGA Gly	ATT Ile	CGA Arg	TCT Ser	TTG Leu	AAA Lys	CTT Leu	GAC Asp	545
				185				190						195		
ATG Met	AAC Ser	CCA Pro	GGC Gly	ACT Thr	GGT Gly	ATC Ile	TGG Trp	CAG Gln	AGT Ser	ATT Ile	GAT Asp	GTG Val	AAG Lys	ACA Thr	GTG Val	590
			200					205					210			
CTG Leu	CAA Gln	AAT Asn	TGG Trp	CTC Leu	AAA Lys	CAG Gln	CCT Pro	GAA Glu	TCC Ser	AAT Asn	TTA Leu	GGC Gly	ATC Ile	GAA Glu	ATA Ile	635
		215					220					225				
AAA Lys	GCT Ala	TTT Phe	GAT Asp	GAG Glu	ACT Thr	GGA Gly	CGA Arg	GAT Asp	CTT Leu	GCT Ala	GTC Val	ACA Thr	TTC Phe	CCA Pro	GGA Gly	680
	230					235					240					
CCA Pro	GGA Gly	GAA Glu	GAT Asp	GGA Gly	TTG Leu	AAC Asn	CCA Pro	TTT Phe	TTA Leu	GAG Glu	GTC Val	AGA Arg	GTT Val	ACA Thr	GAC Asp	725
245					250					255					260	
ACA Thr	CCG Pro	AAA Lys	CGG Arg	TCC Ser	CGC Arg	AGA Arg	GAT Asp	TTT Phe	GGC Gly	CTT Leu	GAC Asp	TGT Cys	GAT Asp	GAG Glu	CAC His	770
				265					270					275		
TCA Ser	ACG Thr	GAA Glu	TCC Ser	CGA Arg	TGT Cys	TGT Cys	CGC Arg	TAC Tyr	CCG Pro	CTG Leu	ACA Thr	GTG Val	GAT Asp	TTC Phe	GAA Glu	815
			280					285					290			
GCT Ala	TTT Phe	GGA Gly	TGG Trp	GAC Asp	TGG Trp	ATT Ile	ATA Ile	GCA Ala	CCT Pro	AAA Lys	AGA Arg	TAC Tyr	AAA Lys	GCC Ala	AAT Asn	860
		295					300					305				
TAC Tyr	TGC Cys	TCC Ser	GGA Gly	GAA Glu	TGC Cys	GAA Glu	TTT Phe	GTG Val	TTT Phe	CTA Leu	CAG Gln	AAA Lys	TAC Tyr	CCG Pro	CAC His	905
	310					315					320					
ACT Thr	CAC His	CTG Leu	GTA Val	CAC His	CAA Gln	GCA Ala	AAT Asn	CCC Pro	AGA Arg	GGC Gly	TCA Ser	GCA Ala	GGC Gly	CCT Pro	TGC Cys	950
325					330					335					340	
TGC Cys	ACA Thr	CCC Pro	ACC Thr	AAG Lys	ATG Met	TCC Ser	CCT Pro	ATA Ile	AAC Asn	ATG Met	CTG Leu	TAT Tyr	TTC Phe	AAT Asn	GGA Gly	995
				345					350					355		
AAA Lys	GAA Glu	CAA Gln	ATA Ile	ATA Ile	TAT Tyr	GGA Gly	AAG Lys	ATA Ile	CCA Pro	GCC Ala	ATG Met	GTT Val	GTA Val	GAT Asp	CGT Arg	1040
			360					365					370			
TGC Cys	GGG Gly	TGC Cys	TCA Ser	TGA												1055
		375														

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

(B) CLONE: Chicken GDF-8

(A) NAME/KEY: Protein

(B) LOCATION: 1..376

(D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

														Met	Gln	Lys	
														1			
Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	Ala	Val	Asp		
5					10					15					20		
Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Glu	Gln	Lys	Glu	Asn	Val	Glu	Lys		
				25					30					35			
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	Lys	Ser	Ser		
			40					45					50				
Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu		
		55					60					65					
Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	Leu	Pro	Lys		
	70					75					80						
Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp		
85					90					95					100		
Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr		
				105					110					11			
Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	Val	Gln	Met		
			120					125					130				
Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln		
		135					140					145					
Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Gln	Val		
	150					155					160						
Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro		
165					170					175					180		
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp		
				185					190					195			
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val		
			200					205					210				
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile		
		215					220					225					
Lys	Ala	Phe	Asp	Glu	Thr	Gly	Arg	Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly		
	230					235					240						
Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	Val	Thr	Asp		
245					250					255					260		
Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His		
				265					270					275			
Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu		
			280					285					290				
Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn		
		295					300					305					
Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His		
	310					315					320						
Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys		
325					330					335							

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Cys Gly Cys Ser
375

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Rat GDF-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...1276
- (D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	ATG ATT CAA AAA	115
	Met Ile Gln Lys	
	1	
CCG CAA ATG TAT GTT TAT ATT TAC CTG TTT GTG CTG ATT GCT GCT GGC	163	
Pro Gln Met Tyr Val Tyr Ile Tyr Leu Phe Val Leu Ile Ala Ala Gly		
5 10 15 20		
CCA GTG GAT CTA AAT GAG GAC AGT GAG AGA GAG GCG AAT GTG GAA AAA	211	
Pro Val Asp Leu Asn Glu Asp Ser Glu Arg Glu Ala Asn Val Glu Lys		
25 30 35		
GAG GGG CTG TGT AAT GCG TGT GCG TGG AGA CAA AAC ACA AGG TAC TCC	259	
Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser		
40 45 50		
AGA ATA GAA GCC ATA AAA ATT CAA ATC CTC AGT AAA CTC CGC CTG GAA	307	
Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu		
55 60 65		
ACA GCG CCT AAC ATC AGC AAA GAT GCT ATA AGA CAA CTT CTG CCC AGA	355	
Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg		
70 75 80		
GCG CCT CCA CTC CGG GAA CTG ATC GAT CAG TAC GAC GTC CAG AGG GAT	403	
Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp		
85 90 95 100		
GAC AGC AGT GAC GGC TCT TTG GAA GAT GAC GAT TAT CAC GCT ACC ACG	451	
Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr		
105 110 115		
GAA ACA ATC ATT ACC ATG CCT ACC GAG TCT GAC TTT CTA ATG CAA GCG	499	
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala		
120 125 130		
GAT GGA AAG CCC AAA TGT TGC TTT TTT AAA TTT AGC TCT AAA ATA CAG	547	
Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln		
135 140 145		

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TAC Tyr 150	AAC Asn 150	AAA Lys 150	GTG Val 150	GTA Val 150	AAG Lys 155	GCC Ala 155	CAG Gln 155	CTG Leu 155	TGG Trp 155	ATA Ile 155	TAT Tyr 160	CTG Leu 160	AGA Arg 160	GCC Ala 160	GTC Val 160	595
AAG Lys 165	ACT Thr 165	CCT Pro 165	ACA Thr 165	ACA Thr 165	GTG Val 170	TTT Phe 170	GTG Val 170	CAA Gln 175	ATC Ile 175	CTG Leu 175	AGA Arg 175	CTC Leu 175	ATC Ile 175	AAA Lys 180	CCC Pro 180	643
ATG Met 185	AAA Lys 185	GAC Asp 185	GGT Gly 185	ACA Thr 185	AGG Arg 185	TAT Tyr 185	ACC Thr 185	GGA Gly 190	ATC Ile 190	CGA Arg 190	TCT Ser 190	CTG Leu 190	AAA Lys 195	CTT Leu 195	GAC Asp 195	691
ATG Met 200	AGC Ser 200	CCA Pro 200	GGC Gly 200	ACT Thr 200	GGT Gly 200	ATT Ile 200	TGG Trp 205	CAG Gln 205	AGT Ser 205	ATT Ile 205	GAT Asp 205	GTG Val 210	AAG Lys 210	ACA Thr 210	GTG Val 210	739
TTG Leu 215	CAA Gln 215	AAT Asn 215	TGG Trp 215	CTC Leu 215	AAA Lys 215	CAG Gln 220	CCT Pro 220	GAA Glu 220	TCC Ser 220	AAC Asn 220	TTA Leu 220	GGC Gly 225	ATT Ile 225	GAA Glu 225	ATC Ile 225	787
AAA Lys 230	GCT Ala 230	TTG Leu 230	GAT Asp 230	GAG Glu 230	AAT Asn 235	GGG Gly 235	CAT His 235	GAT Asp 235	CTT Leu 235	GCT Ala 240	GTA Val 240	ACC Thr 240	TTC Phe 240	CCA Pro 240	GGA Gly 240	835
CCA Pro 245	GGA Gly 245	GAA Glu 245	GAT Asp 245	GGG Gly 245	CTG Leu 250	AAT Asn 250	CCC Pro 250	TTT Phe 250	TTA Leu 250	GAA Glu 255	GTC Val 255	AAA Lys 255	GTA Val 255	ACA Thr 255	GAC Asp 260	883
ACA Thr 265	CCC Pro 265	AAG Lys 265	AGG Arg 265	TCC Ser 265	CGG Arg 265	AGA Arg 265	GAC Asp 265	TTT Phe 270	GGG Gly 270	CTT Leu 270	GAC Asp 270	TGC Cys 270	GAT Asp 270	GAA Glu 275	CAC His 275	931
TCC Ser 280	ACG Thr 280	GAA Glu 280	TCG Ser 280	CGG Arg 280	TGC Cys 280	TGT Cys 280	CGC Arg 280	TAC Tyr 285	CCC Pro 285	CTC Leu 285	ACG Thr 285	GTC Val 285	GAT Asp 290	TTC Phe 290	GAA Glu 290	979
GCC Ala 295	TTT Phe 295	GGA Gly 295	TGG Trp 295	GAC Asp 295	TGG Trp 295	ATT Ile 300	ATT Ile 300	GCA Ala 300	CCC Pro 300	AAA Lys 300	AGA Arg 300	TAT Tyr 305	AAG Lys 305	GCT Ala 305	AAT Asn 305	1027
TAC Tyr 310	TGC Cys 310	TCT Ser 310	GGA Gly 310	GAG Glu 310	TGT Cys 315	GAA Glu 315	TTT Phe 315	GTG Val 315	TTC Phe 315	TTA Leu 315	CAA Gln 320	AAA Lys 320	TAT Tyr 320	CCG Pro 320	CAT His 320	1075
ACT Thr 325	CAT His 325	CTT Leu 325	GTG Val 325	CAC His 325	CAA Gln 330	GCA Ala 330	AAC Asn 330	CCC Pro 330	AGA Arg 330	GGC Gly 335	TCG Ser 335	GCA Ala 335	GGC Gly 335	CCT Pro 340	TGC Cys 340	1123
TGC Cys 345	ACG Thr 345	CCA Pro 345	ACA Thr 345	AAA Lys 345	ATG Met 345	TCT Ser 345	CCC Pro 345	ATT Ile 350	AAT Asn 350	ATG Met 350	CTA Leu 350	TAT Tyr 350	TTT Phe 355	AAT Asn 355	GGC Gly 355	1171
AAA Lys 360	GAA Glu 360	CAA Gln 360	ATA Ile 360	ATA Ile 360	TAT Tyr 360	GGG Gly 365	AAA Lys 365	ATT Ile 365	CCA Pro 365	GCC Ala 365	ATG Met 365	GTA Val 370	GTA Val 370	GAC Asp 370	CGG Arg 370	1219
TGT Cys 375	GGG Gly 375	TGC Cys 375	TCG Ser 375	TGA Ser 375												1276

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: Rat GDF-8

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..376

(D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met 1													Ile	Gln	Lys
Pro	Gln	Met	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Val	Leu	Ile	Ala	Ala	Gly
5					10					15					20
Pro	Val	Asp	Leu	Asn	Glu	Asp	Ser	Glu	Arg	Glu	Ala	Asn	Val	Glu	Lys
				25					30					35	
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn	Thr	Arg	Tyr	Ser
			40					45				50			
Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu
	55						60					65			
Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Arg
	70					75					80				
Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp
85				90						95					100
Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr
				105					110					115	
Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	Met	Gln	Ala
			120					125				130			
Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln
		135					140					145			
Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Ala	Val
	150					155					160				
Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro
165				170					175					180	
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp
				185				190					195		
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val
			200					205				210			
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile
		215					220					225			
Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly
	230					235				240					
Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp
245				250					255						260
Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His
				265				270					275		
Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu
			280					285				290			
Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn
	295					300						305			
Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His
	310					315					320				
Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys
325				330					335					340	

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Turkey GDF-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...1055
- (D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

	ATG CAA AAG	9
	Met Gln Lys	
	1	
CTA GCA GTC TAT GTT TAT ATT TAC CTG TTC ATG CAG ATT TTA GTT CAT	54	
Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile Leu Val His		
5 10 15 20		
CCG GTG GCT CTT GAT GGC AGT AGT CAG CCC ACA GAG AAC GCT GAA AAA	95	
Pro Val Ala Leu Asp Gly Ser Ser Glu Gln Lys Glu Asn Val Glu Lys		
25 30 35		
GAC GGA CTG TGC AAT GCT TGC ACG TGG AGA CAG AAT ACT AAA TCC TCC	140	
Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr Lys Ser Ser		
40 45 50		
AGA ATA GAA GCC ATA AAA ATT CAA ATC CTC AGC AAA CTG CGC CTG GAA	185	
Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu		
55 60 65		
CAA GCA CCT AAC ATT AGC AGG GAC GTT ATT AAA CAA CTT TTA CCC AAA	230	
Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu Leu Pro Lys		
70 75 80		
GCT CCT CCG CTG CAG GAA CTG ATT GAT CAG TAT GAC GTC CAG AGA GAC	275	
Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp		
85 90 95 100		
GAC AGT AGC GAT GGC TCT TTG GAA GAC GAT GAC TAT CAT GCC ACA ACC	320	
Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr		
105 110 115		
GAA ACG ATT ATC ACA ATG CCT ACG GAG TCT GAT TTT CTT GTA CAA ATG	365	
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Val Gln Met		
120 125 130		
GAG GGA AAA CCA AAA TGT TGC TTC TTT AAG TTT AGC TCT AAA ATA CAA	410	
Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln		
135 140 145		
TAT AAC AAA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTG AGG CAA GTC	455	
Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg Gln Val		
150 155 160		

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CAA AAA CCT ACA ACG GTG TTT GTG CAG ATC CTG AGA CTC ATT AAA CCC	500
Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro	
165 170 175 180	
ATG AAA GAC GGT ACA AGA TAT ACT GGA ATT CGA TCT TTG AAA CTT GAC	545
Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys Leu Asp	
185 190 195	
ATG AAC CCA GGC ACT GGT ATC TGG CAG AGT ATT GAT GTG AAG ACA GTG	590
Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys Thr Val	
200 205 210	
TTG CAA AAT TGG CTC AAA CAG CCT GAA TCC AAT TTA GGC ATC GAA ATA	635
Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile	
215 220 225	
AAA GCT TTT GAT GAG AAT GGA CGA GAT CTT GCT GTA ACA TTC CCA GGA	680
Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr Phe Pro Gly	
230 235 240	
CCA GGT GAA GAT GGA CTG AAC CCA TTT TTA GAG GTC AGA GTT ACA GAC	725
Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg Val Thr Asp	
245 250 255 260	
ACA CCA AAA CGG TCC CGC AGA GAT TTT GGC CTT GAC TGC GAC GAG CAC	770
Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His	
265 270 275	
TCA ACG GAA TCT CGA TGT TGT CGC TAC CCG CTG ACA GTG GAT TTT GAA	815
Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu	
280 285 290	
GCT TTT GGA TGG GAC TGG ATT ATA GCA CCT AAA AGA TAC AAA GCC AAT	860
Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn	
295 300 305	
TAC TGC TCT GGA GAA TGT GAA TTC GTA TTT CTA CAG AAA TAC CCG CAC	905
Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His	
310 315 320	
ACT CAC CTG GTA CAC CAA GCA AAT CCA AGA GGC TCA GCA GGC CCT TGC	950
Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys	
325 330 335 340	
TGC ACA CCC ACC AAG ATG TCC CCT ATA AAC ATG CTG TAT TTC AAT GGA	995
Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly	
345 350 355	
AAA GAA CAA ATA ATA TAT GGA AAG ATA CCA GCC ATG GTT GTA GAT CGT	1040
Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg	
360 365 370	
TGC GGG TGC TCA TGA	1055
Cys Gly Cys Ser	
375	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Turkey GDF-8

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..376

(D) OTHER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

												Met	Gln	Lys	
												1			
Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	Leu	Val	His
5					10					15					20
Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Glu	Gln	Lys	Glu	Asn	Val	Glu	Lys
				25					30					35	
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	Lys	Ser	Ser
			40					45				50			
Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu
	55						60					65			
Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	Leu	Pro	Lys
	70					75					80				
Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp
85					90					95					100
Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr
				105					110					115	
Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	Val	Gln	Met
			120					125				130			
Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln
			135				140					145			
Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Gln	Val
	150					155				160					
Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro
165					170					175				180	
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp
				185					190					195	
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val
			200					205				210			
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile
		215					220					225			
Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly
	230					235				240					
Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	Val	Thr	Asp
245					250					255					260
Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	Asp	Glu	His
				265					270					275	
Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu
			280					285				290			
Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn
	295						300					305			
Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	Tyr	Pro	His
	310					315					320				
Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	Pro	Cys
325					330					335					340
Cys	Thr	Pro	Thr	Lys	Met										

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CLAIMS

1. A transgenic non-human animal having a transgene disrupting or interfering with expression of growth differentiation factor-8 (GDF-8) chromosomally integrated into the germ cells of the animal.
2. The transgenic animal of claim 1, wherein the animal is selected from the group of species consisting of avian, bovine, ovine, piscine, murine, and porcine.
3. The transgenic animal of claim 1 where the species is avian.
4. The transgenic animal of claim 1 where the species is bovine.
5. The transgenic animal of claim 1 where the species is porcine.
6. The transgenic animal of claim 1 where the species is ovine.
7. The transgenic animal of claim 1 where the species is piscine.
8. The transgenic animal of claim 1, wherein the transgene comprises GDF-8 antisense polynucleotide(s).
9. The transgenic animal of claim 1, wherein the transgene comprises a gene encoding a dominant negative GDF-8 polypeptide.
10. The transgenic animal of claim 1, wherein the animal is homozygous or heterozygous for GDF-8 polynucleotide.
11. A chicken or turkey egg produced by the transgenic animal of claim 3.

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12. Beef obtained from the transgenic animal of claim 4.
13. Milk obtained from the transgenic animal of claim 4.
14. Pork obtained from the transgenic animal of claim 5.
15. Lamb obtained from the transgenic animal of claim 6.
16. Chicken or turkey meat produced by the transgenic animal of claim 3.
17. A method of producing animal food products having increased muscle mass comprising:
 - a) introducing a transgene disrupting or interfering with expression of growth differentiation factor-8 (GDF-8) into an embryo into germ cells of a pronuclear embryo of the animal;
 - b) implanting the embryo into the oviduct of a pseudopregnant female thereby allowing the embryo to mature to full term progeny;
 - c) testing the progeny for presence of the transgene to identify transgene-positive progeny;
 - d) cross-breeding transgene-positive progeny to obtain further transgene-positive progeny; and
 - e) processing the progeny to obtain foodstuff.
18. The method of claim 17, wherein the transgene comprises GDF-8 antisense polynucleotides.
19. The method of claim 17, wherein the transgene comprises a gene encoding a dominant negative GDF-8 polypeptide.
20. A method of producing avian food products having reduced cholesterol levels comprising:

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- a) introducing a transgene disrupting or interfering with expression of growth differentiation factor-8 (GDF-8) into an embryo of an avian animal;
 - b) culturing the embryo under conditions whereby progeny are hatched;
 - c) testing the progeny for presence of the transgene to identify transgene-positive progeny;
 - d) cross-breeding transgene-positive progeny; and
 - e) processing the progeny to obtain foodstuff.
21. The method of claim 20, wherein the transgene comprises GDF-8 antisense polynucleotides.
22. The method of claim 20, wherein the transgene comprises a gene encoding a dominant negative GDF-8 polypeptide.
23. The transgenic animal of claim 20, wherein the transgene comprises a polynucleotide encoding a truncated GDF-8 polypeptide.
24. A method for increasing the muscle mass in an animal comprising administering to the animal an antibody, or fragment thereof, which binds to GDF-8 polypeptide.
25. The method of claim 24, wherein anti-GDF-8 antibody is administered to a domesticated animal.
26. The method of claim 24, wherein the antibody is a monoclonal antibody or a polyclonal antibody.
27. The method of claim 24, wherein the anti-GDF-8 antibody is administered by intravenous, intramuscular, multiple bolus, or subcutaneous injections.
28. The method of claim 27, wherein the anti-GDF-8 antibody is administered within a dose range of 0.1 ug/kg to 100 mg/kg.

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29. The method of claim 27, wherein the antibody is formulated in a formulation suitable for administration by injection into an animal.
30. A method of inhibiting the growth regulating actions of GDF-8 comprising contacting a GDF-8 agent with fetal or adult muscle cells or progenitor cells.
31. The method of claim 30, wherein the agent is selected from the group consisting of a monoclonal antibody, an antisense nucleic acid and a dominant negative encoding nucleic acid sequence or polypeptide.
32. The method of claim 31, wherein the antibody is a humanized monoclonal antibody or a chimeric monoclonal antibody or fragment thereof.
33. The method of claim 30, wherein the agent is administered to a patient suffering from a disorder selected from the group consisting of muscle wasting disease, neuromuscular disorder, muscle atrophy and aging.
34. The method of claim 30, wherein the agent is administered to a patient suffering from a disorder selected from the group consisting of muscular dystrophy, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS and cachexia.
35. The method of claim 30, wherein the agent is administered to a patient with muscle wasting disease or disorder by intravenous, intramuscular or subcutaneous injection.
36. The method of claim 31, wherein the monoclonal antibody is administered within a dose range between about 0.1/kg to about 100 mg/kg.
37. The method of claim 31, wherein the monoclonal antibody is formulated in a formulation suitable for administration to a patient.

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38. A method for treating a muscle or adipose tissue disorder in a subject, comprising administering a therapeutically effective amount of a GDF-8 agent to the subject, thereby inhibiting abnormal growth of muscle or adipose tissue.
39. The method as in claim 38, wherein the GDF-8 agent is selected from the group consisting of an antisense polynucleotide, a polynucleotide encoding a dominant negative GDF-8 polypeptide, a GDF-8 antibody and a polynucleotide encoding a truncated GDF-8 polypeptide.
40. The method of claim 38, wherein the disorder is a cancer selected from the group consisting of muscle, connective tissue, or bone.
41. The method of claim 38, wherein the subject has an obesity disorder.
42. A method of inhibiting the growth regulating actions of GDF-8 in a subject comprising administering to the subject, a GDF-8 agent that inhibits the action of GDF-8 in the subject.
43. The method of claim 42, wherein the GDF-8 agent is selected from the group consisting of an antisense polynucleotide, a polynucleotide encoding a dominant negative GDF-8 polypeptide, a GDF-8 antibody and a polynucleotide encoding a truncated GDF-8 polypeptide.

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44. A method for identifying a compound that affects GDF-8 activity or gene expression comprising:
- a) incubating the compound with GDF-8 polypeptide, or with a recombinant cell expressing GDF-8 under conditions sufficient to allow the components to interact; and
 - b) determining the effect of the compound on GDF-8 activity or expression.
45. The method of claim 44, wherein the effect is inhibition of GDF-8 activity or expression.
46. The method of claim 44, wherein the effect is stimulation of GDF-8 activity or expression.
47. An isolated polynucleotide encoding a truncated GDF-8 polypeptide wherein the truncation is a loss of the C-terminal active fragment of GDF-8.
48. The isolated polynucleotide of claim 47, wherein the polynucleotide is as shown in FIGURE 12a.

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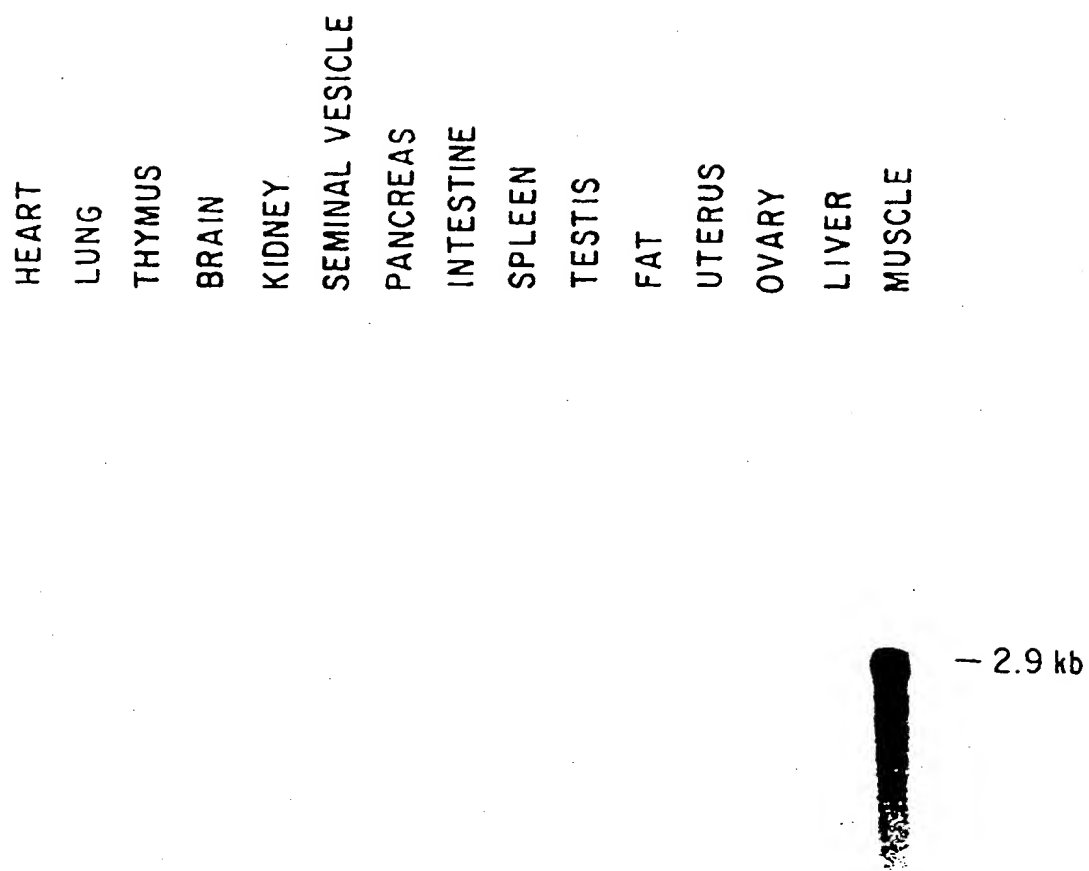


FIG. 1a

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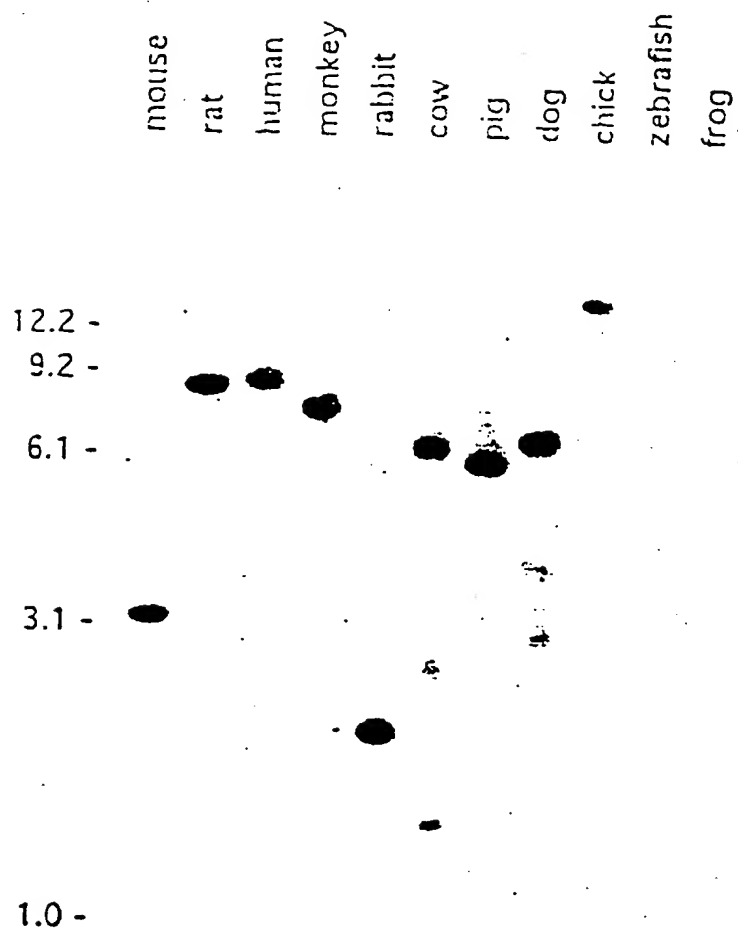


Figure 1b

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1 TTAAGGTAGGAAGGATTT CAGGCTCTATTTACATAATTGTTCTTTCTTTTCACACAGAA 60
N
61 TCCCTTTT TAGAAGTCAAGGTGACAGACACACCCAAGAGGTCCCGGAGAGACTTTGGGCT 120
P F L E V K V T D T P [K R] S [R R] D F G L
121 TGA CTGCGATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCCCTCAGGTCGATTT 180
D C D E H S T E S R C C R Y P L T V D F
181 TGAAGCCTTTGGATGGGACTGGATTATCGCACCCAAAAGATATAAGGCCAATTACTGCTC 240
E A F G W D W I I A P K R Y K A N Y C S
241 AGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCATCTGTGCACCAAGC 300
G E C E F V F L Q K Y P H T H L V H Q A
301 AAACCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAATGTCTCCCATTAATAT 360
N P R G S A G P C C T P T K M S P I N M
361 GCTATATTTAATGGCAAAGAACAATAATATATGGGAAAATCCAGCCATGGTAGTAGA 420
L Y F N G K E Q I I Y G K I P A M V V D
421 CCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTTAGAACTTCCCAAGTCATGGAAGGTC 480
R C G C S *
481 TTCCCTCAATTTCCGAAACTGTGAATTCCTGCAGCCCGGGGATCCACTAGTTCTAGAGC 540
541 GGCCGCCACC 550

FIG.2a

1 CAAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCAGGAT 60
[K R] S [R R] D F G L D C D E H S T E S R C
61 GCTGTGTTACCCCTCTAACTGTGATTTTGAAGCTTTTGGATGGGATTGCGATTATCGCTC 120
C R Y P L T V D F E A F G W D W I I A P
121 CTAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGTATTTTACAAAAAT 180
K R Y K A N Y C S G E C E F V F L Q K Y
181 ATCCTCATACTCATCTGGTACACCAAGCAAACCCAGAGGTTACAGCAGGCCCTTGCTGTA 240
P H T H L V H Q A N P R G S A G P C C T
241 CTCCCACAAAGATGTCTCCAATTAATATGCTATATTTAATGGCAAAGAACAATAATAT 300
P T K M S P I N M L Y F N G K E Q I I Y
301 ATGGGAAAATCCAGCGATGGTAGTA 326
G K I P A M V V

FIG.2b

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GAA GAT GGG CTG AAT CCC TTT TTA GAA GTC AAA GTA ACA GAC ACA CCC AAG AGG TCC CGG
 E D G L N P F L E V K V T D T P K R S R
 AGA GAC TTT GGG CTT GAC TGT GAT GAA CAC TCC ACG GAA TCG CGG TGC TGT CGC TAC CCC
 R D F G L D C D E H S T E S R C C R Y P
 CTC AAG GTC GAT TTC GAA GCC TTT GGA TGG GAC TGG ATT ATT GCA CCC AAA AGA TAT AAG
 L T V D F E A F G W D W I I A P K R Y K
 GCT AAT TAC TGC TCT GGA GAG TGT GAA TTT GTG TTC TTA CAA AAA TAT CCG CAT ACT CAT
 A N Y C S G E C E F V F L Q K Y P H T H
 CTT GTG CAC CAA GCA AAC CCC AGA GGC TCG GCA GGC CCT TGC TGC ACG CCA ACA AAA ATG
 L V H Q A N P R G S A G P C C T P T K M
 TCT CCC ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA TAT GGG AAA ATT CCA
 S P I N M L Y F N G K E Q I I Y G K I P
 GCC ATG GTA GTA GAC CGG TGT GGG TGC TCG TGA GCT TTG CAT TAG CTT TAA AAT TTC CCA
 A M V V D R C G C S
 AAT CGT GGA AGG TCT TCC CCT CGA TTT CGA AAC TGT GAA TTT ATG TAC CAC AGG CTG TAG

Rat GDF-8

FIG. 2c

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TTA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTG AGG CAA GTC CAA AAA CCT ACA ACG GTG
L V V K A Q L W I Y L R Q V Q K P T T V

TTT GTG CAG ATC CTG AGA CTC ATT AAG CCC ATG AAA GAC GGT ACA AGA TAT ACT GGA ATT
F V Q I L R L I K P M K D G T R Y T G I

GGA TCT TTG AAA CTT GAC ATG AAC CCA GGC ACT GGT ATC TGG CAG AGT ATT GAT GTG AAG
G S L K L D M N P G T G I W Q S I D V K

ACA GTG CTG CAA AAT TGG CTC AAA CAG CCT GAA TCC AAT TTA GGC ATC GAA ATA AAA GCT
T V L Q N W L K Q P E S N L G I E I K A

TTT GAT GAG ACT GGA CGA GAT CTT GCT GTC ACA TTC CCA GGA CCG GGT GAA GAT GGA TTG
F D E T G R D L A V T F P G P G E D G L

AAC CCA TTT TTA GAG GTC AGA GTT ACA GAC ACA CCG AAA CGG TCC CGC AGA GAT TTT GCC
N P F L E V R V T D T P K R S R R D F G

CTT GAC TGT GAT GAG CAC TCA ACG GAA TCC CGA TGT TGT CGC TAC CCG CTG ACA GTG GAT
L D C D E H S T E S R C C R Y P L T V D

TTC GAA GCT TTT GGA TGG GAC TGG ATT ATA GCA CCT AAA AGA TAC AAA GCC AAT TAC TGC
F E A F G W D W I I A P K R Y K A N Y C

TCC GGA GAA TGC GAA TTT GTG TTT CTA CAG AAA TAC CCG CAC ACT CAC CTG GTA CAC CAA
S G E C E F V F L Q K Y P H T H L V H Q

GCA AAT CCC AGA GGC TCA GCA GGC CCT TGC TGC ACA CCC ACC AAG ATG TCC CCT ATA AAC
A N P R G S A G P C C T P T K M S P I N

ATG CTG TAT TTC AAT GGA AAA GAA CAA ATA ATA TAT GGA AAG ATA CCA GCC ATG GTT GTA
M L Y F N G K E Q I I Y G K I P A M V V

GAT CGT TGC GGG TGC TCA TGA GGC TGT CGT GAG ATC CAC CAT TCG ATA AAT TGT GGA AGC
D R C G C S

CAC CAA AAA AAA AAG CTA TAT CCC CTC ATC CAT CTT TGA AAC TGT GAA ATT ACG TAC GCT

AGG CAT TGC C

Chicken GDF-8

FIG. 2d

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GDF-8 SRROFGLCDDEHSTESRCRYPLTVDF-EAFGWD-WI IAPKRYKANYSGECFVFLQKYP—
 GDF-1 RPRRDAEPVLGGPGGACRARRLYVSF-REVGWHRWV IAPRGFLANYCGGCCALPVALSGSGGPP
 BMP-2 REKROAKHKORKRLKSSCKRHPLVYDF-SDVGWNDWI VAPPGYHAFYCHGECFPLADHLNS—
 BMP-4 KRSPKHHSQRARKKNKNCRRHSLYVDF-SDVGWNDWI VAPPGYQAFYCHGDCPFPLADHLNS—
 Vgr-1 SRSGSSDYNGSELKTACKKHEL YVSF-QDLGWQDWI IAPKGYAANYCGECFPLNAHMNA—
 OP-1 LRMANVAENSSSDQROACKKHEL YVSF-RDLGWQDWI IAPEGYAANYCGECFPLNSYMNA—
 BMP-5 SRMSSVGDYNTSEKQACKKHEL YVSF-RDLGWQDWI IAPEGYAANYCGECFPLNAHMNA—
 BMP-3 EQTLKKARRKQWIEPRNCARRYLKVDFA-DIGWSEW I I SPKSFDAAYCSGACQFPMPSLKPS—
 MIS GPGRAQRSAGATAADGPCALRELSVDL—RAERSVL I PETYQANNCGVCGWQSDRNPRY—
 Inhibin α ALRLLQRPPEEPAHANCHRYVALNISF-QELGWERWIVYPPSF IFHYCHGGGLHIPPNLSLPV-
 Inhibin β A HRRRRRGLECDGKV-NICCKKQFFVSF-KDIGWNDWI IAPSGYHANYCGECFPLACTSGSSL-
 Inhibin β B HRIRKRGLECDGRT-NLCCRQOFFIDF-RLIGWNDWI IAPTGYGNYCEGSCPAYLAGVPGSAS-
 TGF- β 1 HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD—
 TGF- β 2 KKRALDAAYCFRNVDNCCRLPLYIDFRKDLGWK-WIHEPKGYNANFAGACPYLWSSD—
 TGF- β 3 KKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWK-WIHEPKGYANFQSGPCPYLRSAD—

GDF-8 -HTHLVHQANPRG—SAGPCCT-PTKMSPINMLYF-NGKEQI IYGKIPAMVVDRCCGS
 GDF-1 ALNHAVLRALMHA-AAPGAADLPCCV-PARLSPISVLFF-DNSDNVVLROYEDMNVDECCOR
 BMP-2 -TNHAI VQTLVNS—VNSKIPKACCV-PTELSAISMLYL-DENEKVVLKNYQDMVVEGCCOR
 BMP-4 -TNHAI VQTLVNS—VNSSIPKACCV-PTELSAISMLYL-DEYDKVVLKNYQDMVVEGCCOR
 Vgr-1 -TNHAI VQTLVHL—INPEYVPKPCA-PTKLNAISVLYF-DDNSNVILKKYRNMVVRACCOH
 OP-1 -TNHAI VQTLVHF—INPETVPKPCA-PTQLNAISVLYF-DDSSNVILKKYRNMVVRACCOH
 BMP-5 -TNHAI VQTLVHL—MFPDHVPKPCA-PTKLNAISVLYF-DDSSNVILKKYRNMVVRACCOH
 BMP-3 -NHATIQSIVRA-VGVVPGIPEPCOV-PEKMSSLSILFF-DENKNVVLKVYPNMTVE SCAOR
 MIS -GNHVVL LLLKMQA-RGAALARPPCOV-PTAYAGKLL ILSSEER—ISAHVPMNVATECCOR
 Inhibin α -PGAPPTPAQPY—LLPGAQPCOALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCAQI
 Inhibin β A -SFHSTVINHYRMRGHSFANLKSCOV-PTKLRPMSMLY-DDGQNI IKKDIQNMIVECCGS
 Inhibin β B -SFHTAVVNQYRMRLNPGT-VNSCCI—PTKLSTMSMLYF-DDEYNIVKROVPMIIVECCGA
 TGF- β 1 -TOYSKVLALYNQ-HNPGASAAPCOV-POALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
 TGF- β 2 -TQHSRVLSLYNT-INPEASASPCOV-SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCCKS
 TGF- β 3 -TTHSTVLGLYNT-LNPEASASPCOV-PQDLEPLTILYY-VGRTPKV-EQLSNMIVKSCCKS

FIG.3a

1	human	HOKLOLCVYIYLFHLIVAGPVDDLNSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKRLRETAPNISKDV	80
	murine	HHOKLOMYVYIYLFHLIAAGPVDDLNEGSEREENVEKEGLCNACAWRQNTKSSRIEAIKIQILSKRLRETAPNISKDA	IRQ
	rat		
	chicken		
81	human	LLPKAPPLRELIDQDVORDDSSDGSLEDDDDYHATTETIIITMPTESDEFLMQVDQPKKCCFPKPSBKIQYNKKVUKAQLWIY	160
	murine	LLPKRAPPLRELIDQDVORDDSSDGSLEDDDDYHATTETIIITMPTESDPLMQADQPKKCCFPKPSBKIQYNKKVUKAQLWIY	
	rat		
	chicken	LUVKAQLWIY	
161	human	LRPVEPTTTFVVOILRLIKPHKDGTRYTGIRSLKLDNPNPGTGIWOSIDVKTVLQNLWKQSPESNLGIEIKALDENGHD	240
	murine	LRPVKTPTTTFVVOILRLIKPHKDGTRYTGIRSLKLDNPNPGTGIWOSIDVKTVLQNLWKQSPESNLGIEIKALDENGHD	LAV
	rat		
	chicken	LRQVQKPTTTFVVOILRLIKPHKDGTRYTGISLKLDDNPNPGTGIWOSIDVKTVLQNLWKQSPESNLGIEIKAFDETGR	DLAV
241	human	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFPV	320
	murine	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFPV	PLO
	rat	EDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFPV	PLO
	chicken	TFPGPGEDGLNPFLEVRVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFPV	PLO
321	human	KYPHTHLVHQANPRGSAGPCCCTPTKHSPIINMLYFNGKEQIIYGKIPAMVVDR	376
	murine	KYPHTHLVHQANPRGSAGPCCCTPTKHSPIINMLYFNGKEQIIYGKIPAMVVDR	CGCS
	rat	KYPHTHLVHQANPRGSAGPCCCTPTKHSPIINMLYFNGKEQIIYGKIPAMVVDR	CGCS
	chicken	KYPHTHLVHQANPRGSAGPCCCTPTKHSPIINMLYFNGKEQIIYGKIPAMVVDR	CGCS

FIG. 3b

[illegible]

FIG. 4

1 GTCTCTCGGACGGTACATGCACTAATATTTCACTTGGCATTACTCAAAGCAAAAAGAAG 60
61 AAATAAGAACAAGGGAAGAAAAAAGATTGTGCTGATTTTTAAATGATGCAAAACTGCA 120
M M Q K L Q
121 AATGTATGTTTATATTTACCTGTTTCATGCTGATTGCTGCTGCCCCAGTGGATCTAAATGA 180
M Y V Y I Y L F M L I A A G P V D L N E
181 GGGCAGTGACAGAGAAGAAATGTGGAAAAAGAGGGCTGTGTAATGCATGTCCGTGGAG 240
G S E R E E N V E K E G L C N A C A W R
241 ACAAACACGAGGTACTCCAGAATAGAAGCCATAAAATTCAAATCCTCAGTAAGCTGCC 300
Q N T R Y S R I E A I K I Q I L S K L R
301 CCTGGAACAGCTCCTAACATCAGCAAAGATGCTATAAGACAACCTCTGCCAAGAGCGCC 360
L E T A P N I S K D A I R Q L L P R A P
361 TCCACTCCGGAAGTATGATCAGTACGACGTCCAGAGGGATGACAGCAGTATGGCTC 420
P L R E L I D Q Y D V Q R D D S S D G S
421 TTTGGAAGATGACGATTATCAGCTACCACGGAACAATCATTACCATGCCTACAGAGTC 480
L E D D D Y H A T T E T I I T M P T E S
481 TGACTTTCTAATGCAAGCGGATGGCAAGCCCAATGTTGCTTTTTAAATTTAGCTCTAA 540
D F L M Q A D G K P K C C F F K F S S K
541 AATACAGTACAACAAAGTAGTAAAGCCCAACTGTGGATATATCTCAGACCCGTCAAGAC 600
I Q Y N K V V K A Q L W I Y L R P V K T
601 TCCTACAACAGTGTTTGTGCAAATCCTGAGACTCATCAACCCATGAAAGACGGTACAAG 660
P T T V F V Q I L R L I K P M K D G T R
661 GTATACTGGAATCCGATCTCTGAACTTGACATGAGCCCAGGCACTGGTATTTGGCAGAG 720
Y T G I R S L K L D M S P G T G I W Q S
721 TATTGATGTGAAGACAGTGTGCAAAATTTGGCTCAAACAGCCTGAATCCAACCTTAGGCAT 780
I D V K T V L Q N W L K Q P E S N L G I
781 TGAAATCAAAGCTTTGATGAGAATGGCCATGATCTTGCTGTAACCTCCCAGGACCAGG 840
E I K A L D E N G H D L A V T F P G P G
841 AGAAGATGGGCTGAATCCCTTTTAGAAGTCAAGGTGACAGACACACCAAGAGGTCCCG 900
E D G L N P F L E V K V T D T P K R S R
901 GAGAGACTTTGGGCTTGACTGGCATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCC 960
R D F G L D C D E H S T E S R C C R Y P
961 CCTCAGGTCGATTTTGAAGCCTTTGGATGGGACTGGATTATCGACCCAAAAGATATAA 1020
L T V D F E A F G W D W I I A P K R Y K
1021 GGCCAATTACTGCTCAGGAGAGTGTGAATTTGTGTTTTTACAAAATATCCGCATACTCA 1080
A N Y C S G E C E F V F L Q K Y P H T H
1081 TCTTGTGCACCAAGCAAACCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAAT 1140
L V H Q A N P R G S A G P C C T P T K M
1141 GTCTCCCATTAATATGCTATATTTAATGCCAAAGAACAATAATATATGGGAAAATTCC 1200
S P I N M L Y F N G K E Q I I Y G K I P
1201 AGCCATGGTAGACCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTAGAACTTCCC 1260
A M V V D R C G C S *

FIG.5a

1261 AAGTCATGGAAGGCTCTCCCTCAATTCGAAACTGTGAATTCAGCACCACAGGCTGTA 1320
1321 GGCCTTGAGTATGCTCTAGTAACGTAAGCACAAGCTACAGTGTATGAACAAAAGAGAGA 1380
1381 ATAGATGCAATGGTTGGCATTCAACCACAAAATAAACCATACTATAGGATGTTGTATGA 1440
1441 TTTCCAGAGTTTTGAAATAGATGGAGATCAAATTACATTTATGTCCATATATGTATATT 1500
1501 ACAACTACAATCTAGGCAAGGAAGTGAGAGCACATCTTGTGGTCTGCTGAGTTAGGAGGG 1560
1561 TATGATTAAGGTAAGTCTTATTTCTAACAGTTTCACTTAATTTACAGAAGAATC 1620
1621 TATATGTAGCCTTGTAAAGTGTAGGATTGTTATCATTTAAAAACATCATGTACACTTAT 1680
1681 ATTTGTATTGTATACTTGGTAAGATAAAATTCACAAAGTAGGAATGGGGCTCACATAC 1740
1741 ACATTGCCATTCTATTATAATTGGACAATCCACCACGGTGCTAATGCAGTCTGAATGG 1800
1801 CTCCTACTGGACCTCTCGATAGAACACTCTACAAAGTACGAGTCTCTCTCTCCCTCCAG 1860
1861 GTGCATCTCCACACACACAGCACTAAGTGTTCAATGCATTTTCTTTAAGGAAAGAAGAAT 1920
1921 CTTTTTTCTAGAGGTCAACTTTCAGTCAACTCTAGCACAGCGGGAGTGACTGCTGCATC 1980
1981 TTAAAAGGCAGCCAAACAGTATTCATTTTTTAATCTAAATTTCAAAATCACTGCTGCCT 2040
2041 TTATCACATGGCAATTTTGTGGTAAATAATGGAAATGACTGGTTCTATCAATATTGTAT 2100
2101 AAAAGACTCTGAAACAATTACATTTATATAATGTATACAATATTGTTTTGTAAATAAG 2160
2161 TGTCTCCTTTTATATTTACTTTGGTATATTTTACACTAATGAAATTTCAAATCATTAAA 2220
2221 GTACAAAGACATGTCATGTATCACAAAAAGGTGACTGCTTCTATTTAGAGTGAATTAG 2280
2281 CAGATTCAATAGTGGTCTTAAACTCTGTATGTTAAGATTAGAAGGTTATATTACAATCA 2340
2341 ATTTATGTATTTTTACATTATCAACTTATGGTTTCATGGTGGCTGTATCTATGAATGTG 2400
2401 GCTCCAGTCAAATTTCAATGCCCCACCATTTTAAAAATTACAAGCATTACTAAACATAC 2460
2461 CAACATGTATCTAAAGAAATACAAATATGGTATCTCAATAACAGCTACTTTTTATTTTA 2520
2521 TAATTTGACAATGAATACATTTCTTTTATTTACTTCAGTTTTATAAATTGGAACCTTTGTT 2580
2581 TATCAATGTATTGTACTCATAGCTAAATGAAATTATTTCTTACATAAAATGTGTAGAA 2640
2641 ACTATAAATTAAGTGTTCACATTTTGAAGGC 2676

FIG.5b

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1 AAGAAAAGTAAAAGGAAGAAACAAGAACAAGAAAAAGATTATATTGATTTTAAAATCAT 60
M
61 GCAAAAAGTGAACCTCTGTGTTTATATTACCTGTTTATGCTGATTGTTGCTGGTCCAGT 120
Q K L Q L C V Y I Y L F M L I V A G P V
121 GGATCTAAATGAGAACAGTGAACAAAAAGAAATGTGCAAAAAGAGGGCTGTGTAATGC 180
D L N E N S E Q K E N V E K E G L C N A
181 ATGTACTTGGAGACAAAACACTAAATCTTCAAGAATAGAAGCCATTAAGATACAAATCCT 240
C T W R Q N T K S S R I E A I K I Q I L
241 CACTAAACTTCGTCTGGAACAGCTCCTAACATCAGCAAAGATGTTATAAGACAACCTTT 300
S K L R L E T A P **N I S** K D V I R Q L L
301 ACCCAAAGCTCCTCCACTCCGGGAAGTATTGATCAGTATGATGCCAGAGGGATGACAG 360
P K A P P L R E L I D Q Y D V Q R D D S
361 CAGCGATGGCTCTTTGGAAGATGACGATTATCAGCTACAACGGAACAATCATTACCAT 420
S D G S L E D D D Y H A T T E T I I T M
421 GCCTACAGAGTCTGATTTTCTAATGCAAGTGGATGCAAAACCCAAATGTTGCTTCTTTAA 480
P T E S D F L M Q V D G K P K C C F F K
481 ATTTAGCTCTAAAATACAATAACAATAAGTAGTAAAGGCCCAACTATGGATATATTGAG 540
F S S K I Q Y N K V V K A Q L W I Y L R
541 ACCCGTCGAGACTCCTACAACAGTGTGTTGTGCAAACTCCTGAGACTCATCAACCTATGAA 600
P V E T P T T V F V Q I L R L I K P M K
601 AGACGGTACAAGGTATACTGGAATCCGATCTCTGAACTTGACATGAACCCAGGCACTGG 660
D G T R Y T G I R S L K L D M N P G T G
661 TATTTGGCAGAGCATTGATGTGAAGACAGTGTGCAAAATGGCTCAAACAACCTGAATC 720
I W Q S I D V K T V L Q N W L K Q P E S
721 CAACTTAGGCATTGAAATAAAGCTTTAGATGAGAATGGTCATGATCTTGCTGTAACTT 780
N L G I E I K A L D E N G H D L A V T F
781 CCCAGGACCAGGAGAAGATGGGCTGAATCCGTTTTTAGAGGTCAAGGTAACAGACACACC 840
P G P G E D G L N P F L E V K V T D T P
841 AAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCAGGATG 900
K **R S R R** D F G L D C D E H S T E S R C
901 CTGTCGTTACCTCTAACTGTGGATTTTGAAGCTTTTGGATGGGATTGGATTATCGCTCC 960
C R Y P L T V D F E A F G W D W I I A P
961 TAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGATTTTTACAAAATA 1020
K R Y K A N Y C S G E C E F V F L Q K Y
1021 TCCTCATACTCATCTGGTACCAAGCAAAACCCAGAGGTTACAGAGGCCCTTGCTGTAC 1080
P H T H L V H Q A N P R G S A G P C C T
1081 TCCCACAAGATGTCTCCAATTAATATGCTATATTTAATGGCAAAGAACAATAATATA 1140
P T K M S P I N M L Y F N G K E Q I I Y
1141 TGGGAAAATTCCAGCGATGGTAGACCGCTGTGGGTGCTCATGAGATTTATATTAAGC 1200
G K I P A M V V D R C G C S *

FIG.5c

1201 GTTCATAACTTCCTAAAACATGGAAGGTTTTCCCTCAACAATTTGAAGCTGTGAAATT 1260
1261 AAGTACCACAGGCTATAGGCCTAGAGTATGCTACAGTCACTTAAGCATAAGCTACAGTAT 1320
1321 GTAAACTAAAAGGGGAATATATGCAATGGTTGGCATTTAACCATCCAAACAAATCATA 1380
1381 AAGAAAGTTTTATGATTTCCAGAGTTTTTGAGCTAGAAGGAGATCAAATTACATTTATGT 1440
1441 TCCTATATATTACAACATCGGCGAGGAAATGAAAGCGATTCTCCTTGAGTTCTGATGAAT 1500
1501 TAAAGGAGTATGCTTTAAAGTCTATTTCTTTAAAGTTTTGTTTAAATTTACAGAAAAAT 1560
1561 CCACATACAGTATTGGTAAAATGCAGGATTGTTATATACCATCATTCGAATCATCCTTAA 1620
1621 ACACCTGAATTTATATTGTATGGTAGTATACTTGGTAAGATAAAATCCACAAAAATAGG 1680
1681 GATGGTGCAGCATATGCAATTTCCATTCTATTATAATTGACACAGTACATTAACAATCC 1740
1741 ATGCCAACGGTGCTAATACGATAGGCTGAATGCTGAGGCTACCAGGTTTATCACATAAA 1800
1801 AAACATTCAGTAAATAGTAAGTTCTCTTTCTTCAGGTGCATTTTCCTACACCTCCAA 1860
1861 ATGAGGAATGGATTTTCTTTAATGTAAGAAGAATCATTTTTCTAGAGGTTGGCTTTCAAT 1920
1921 TCTGTAGCATACTTGGAGAACTGCATTATCTTAAAAGGCAGTCAAATGGTGTGTTGTTT 1980
1981 TATCAAAATGTCAAAATAACATACTTGGAGAAGTATGTAATTTTGCTTTGGAAAATTAC 2040
2041 AACACTGCCTTTGCAACACTGCAGTTTTATGGTAAAATAATAGAAATGATCGACTCTAT 2100
2101 CAATATTGTATAAAAAGACTGAAACAATGCATTATATAATATGTATACAATATTGTTTT 2160
2161 GTAAATAAGTGCTCCTTTTTTATTTACTTTGGTATATTTTACACTAAGGACATTTCAA 2220
2221 ATTAAGTACTAAGGCACAAAGACATGTCATGCATCACAGAAAAGCAACTACTTATATTTC 2280
2281 AGAGCAAATTAGCAGATTAAATAGTGGTCTTAAACTCCATATGTTAATGATTAGATGGT 2340
2341 TATATTACAATCATTTTATATTTTTTACATGATTAAACATTCATTATGGATTATGATG 2400
2401 GCTGTATAAAGTGAATTTGAAATTTCAATGGTTTACTGTCATTGTGTTAAATCTCAACG 2460
2461 TTCCATTATTTAATACTTGCAAAAACATTACTAAGTATACCAAAATAATTGACTCTATT 2520
2521 ATCTGAAATGAAGAATAAACTGATGCTATCTCAACAATAACTGTTACTTTTATTTTATAA 2580
2581 TTTGATAATGAATATATTTCTGCATTTATTTACTTCTGTTTTGTAATTTGGGATTTGTT 2640
2641 AATCAAAATTTATGTACTATGACTAAATGAAATTATTTCTTACATCTAATTTGTAGAAAC 2700
2701 AGTATAAGTTATATTAAAGTGTTTTACATTTTTTTGAAAGAC 2743

FIG.5d

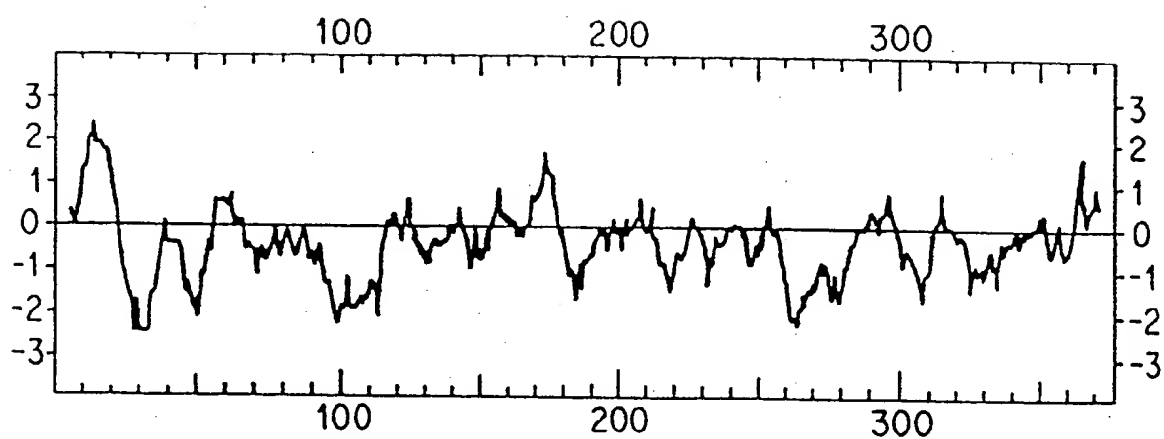


FIG. 6a

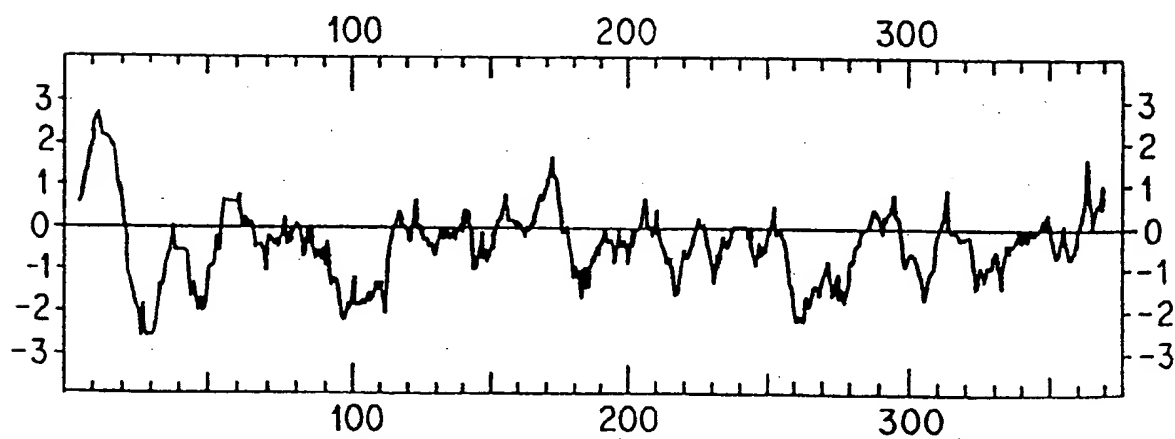
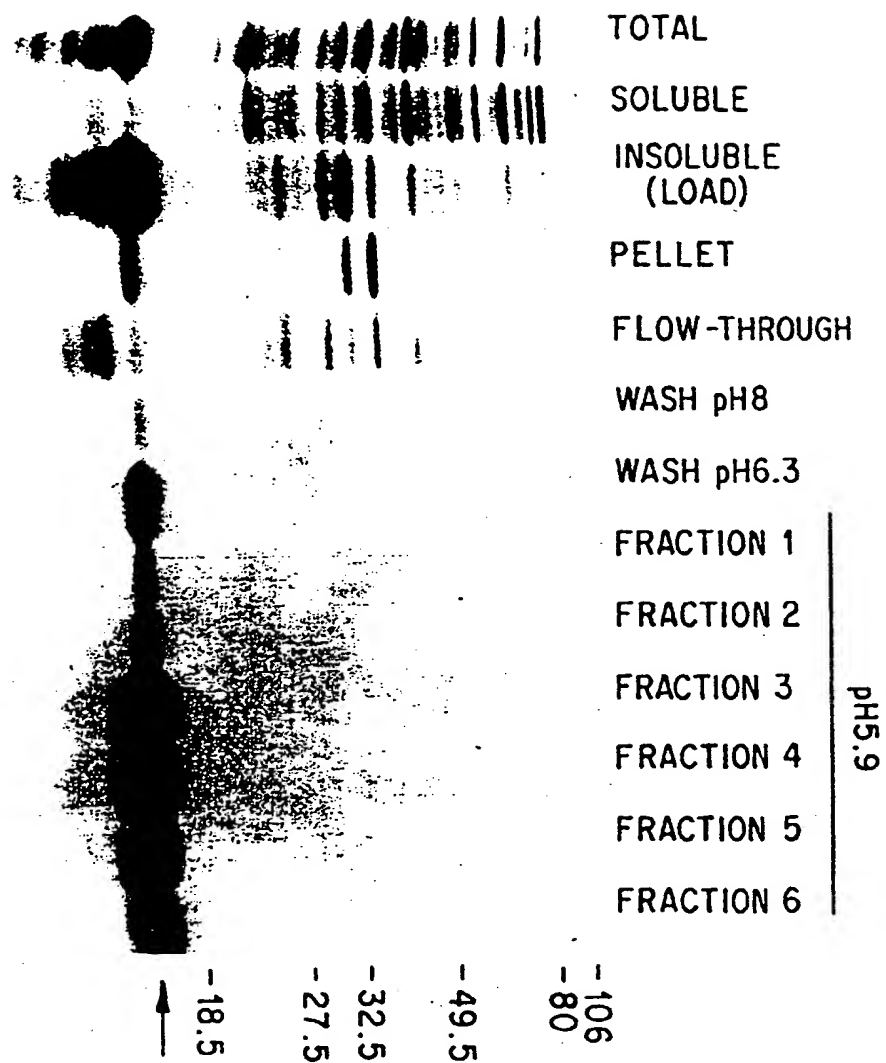


FIG. 6b

FIG. 8



ANTISENSE SENSE

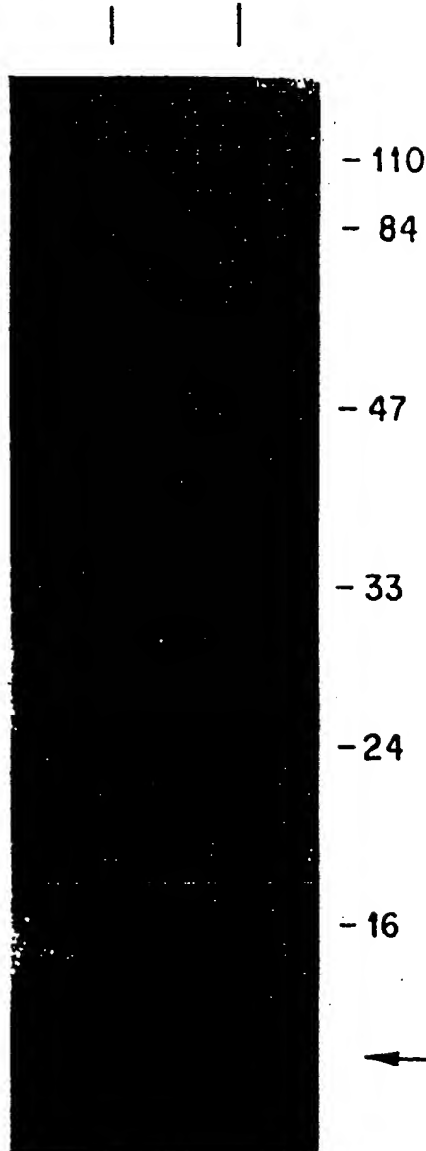


FIG. 9

FIG. 10A

HEART
LUNG
THYMUS
BRAIN
KIDNEY
SEMINAL VESICLE
PANCREAS
INTESTINE
SPLEEN
TESTIS
MUSCLE
LIVER
OVARY
FAT
UTERUS

- 2.9 kb

18/32

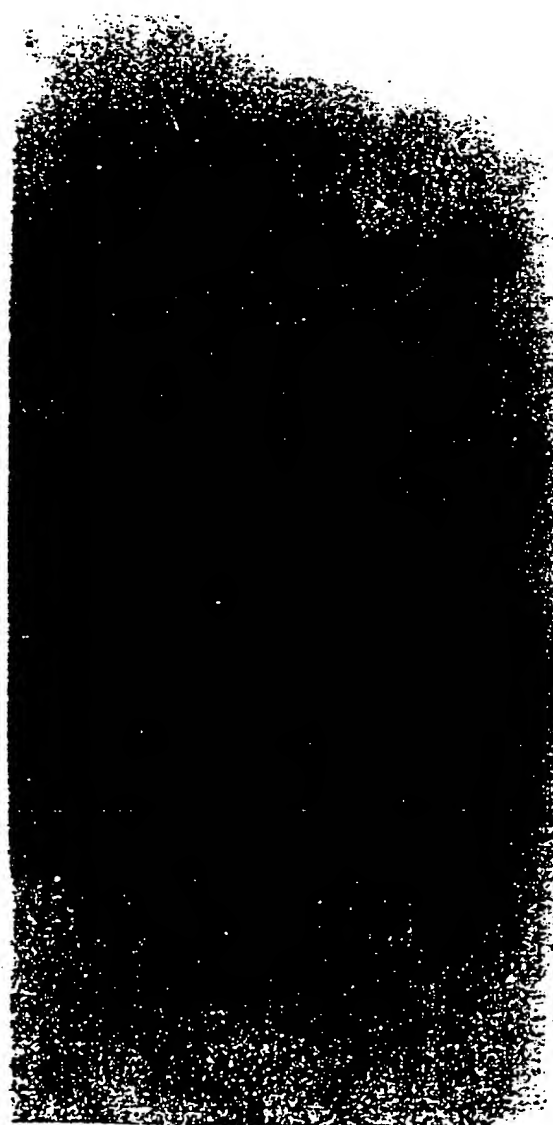
12.5 d PLACENTA

14.5 d PLACENTA

16.5 d PLACENTA

12.5 d EMBRYO

18.5 d EMBRYO



-2.9 kb

FIG. 10b

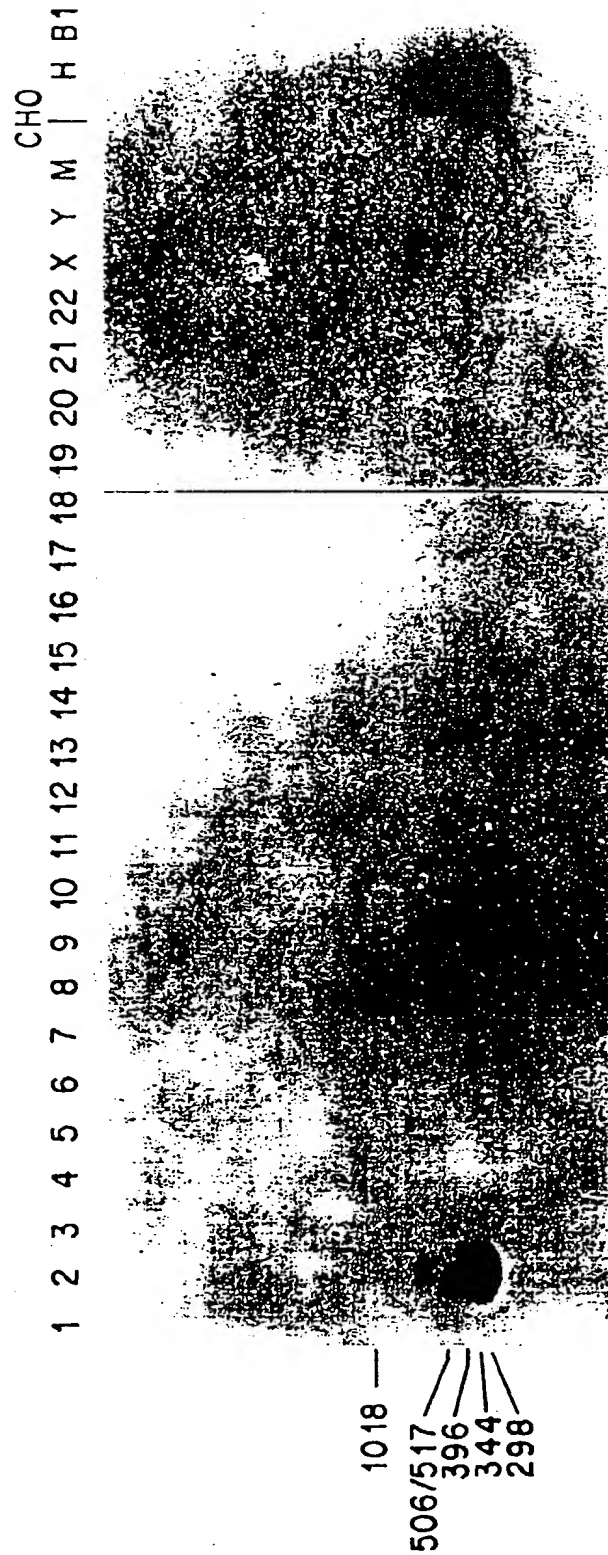


FIG.11

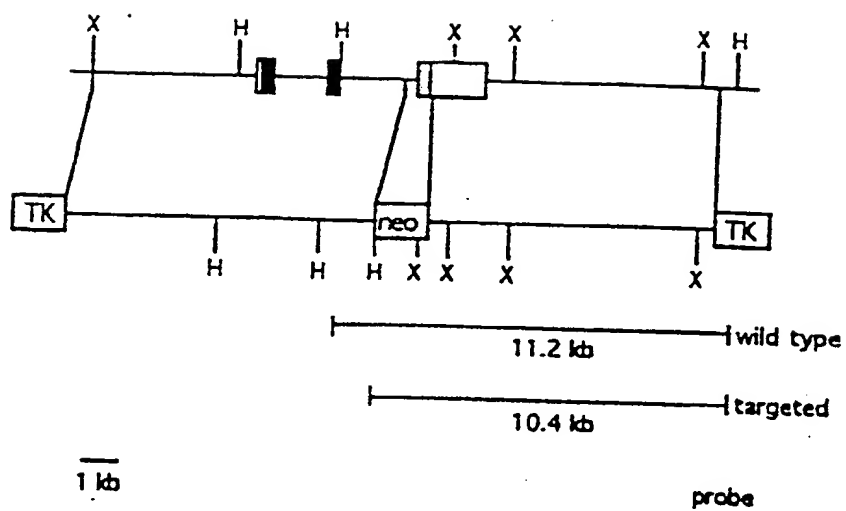


Figure 2a

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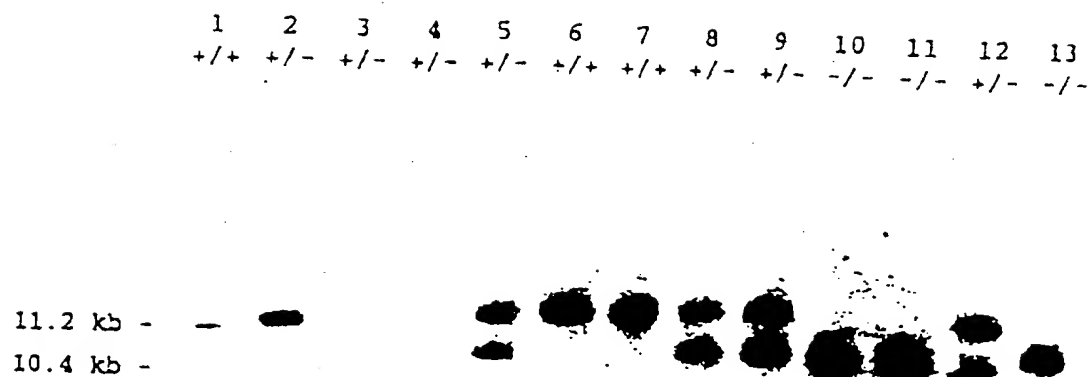


Figure 12b

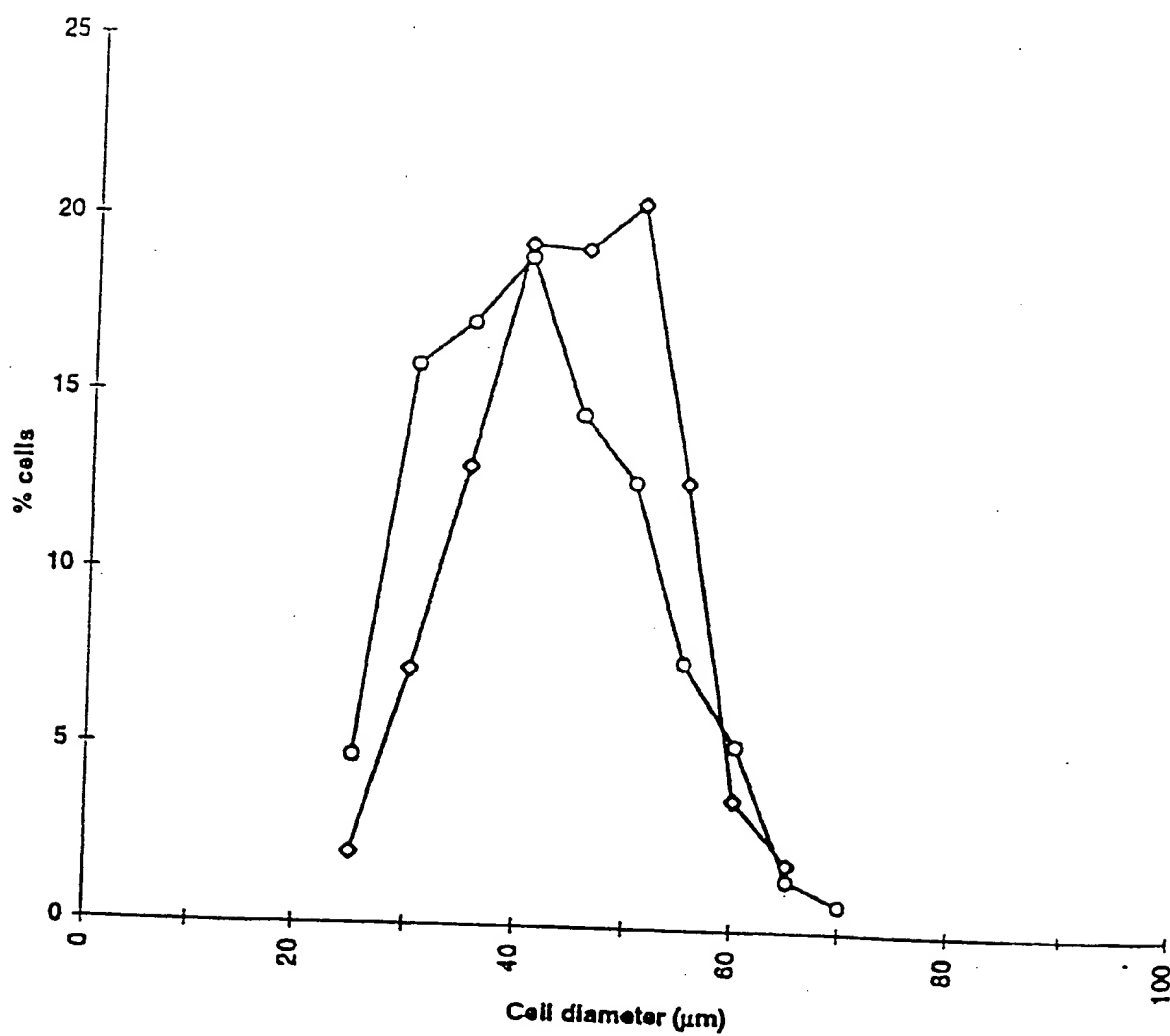


Figure 3a
bottom

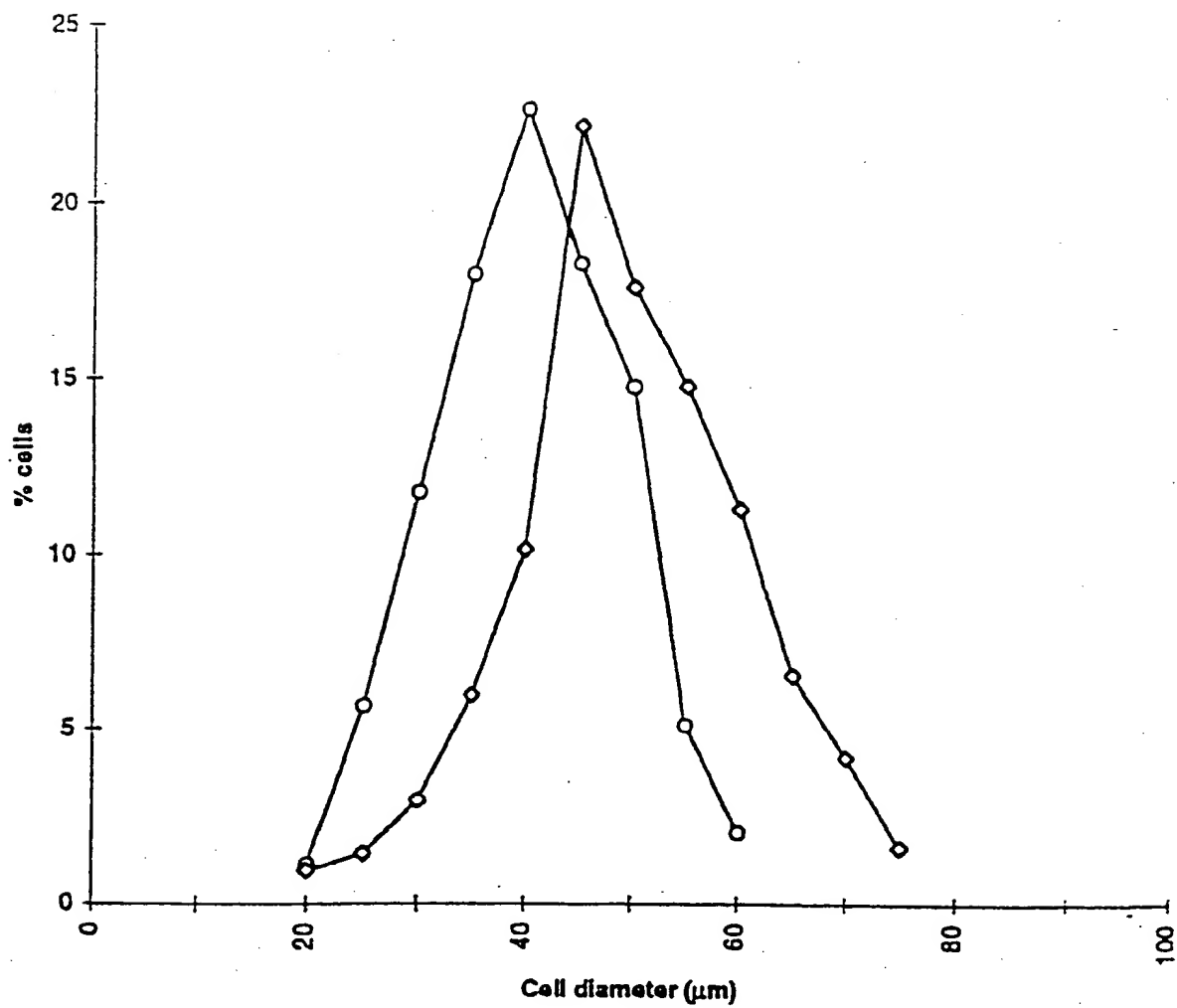


Figure 13b
bottom

FIGURE 14a

```

1/1                               31/11
ATG CAA AAA CTG CAA CTC TGT GTT TAT ATT TAC CTG TTT ATG CTG ATT GTT GGT GGT CCA
M Q K L Q L C V Y I Y L F M L I V A G P
61/21                               91/31
GTG GAT CTA AAT GAG AAC ACT GAG CAA AAA GAA AAT GTG GAA AAA GAG GGG CTG TGT AAT
V D L N E N S E Q K E N V E K E G L C N
121/41                               151/51
GCA TGT ACT TGG AGA CAA AAC ACT AAA TCT TCA AGA ATA GAA CCC ATT AAA ATA CAA ATC
A C T W R C N T K S S R I E A I K I Q I
181/61                               211/71
CTC AGT AAA CTT COT CTG GAA ACA GGT COT AAC ATC AGC AAA GAT GCT ATA AGA CAA CTT
L S K L R L E T A P N I S K D A I R Q L
241/81                               271/91
TTA CCC AAA GGT COT CCA CTC CGG GAA CTG ATT GAT CAG TAT GAT GTC CAG AGG GAT GAC
L P K A P P L R E L I D Q Y D V Q R D D
301/101                               331/111
AGC AGC GAT GGC TGT TGG CAA GAT GAC GAT TAT CAC GGT ACA ACG GAA ACA ATC ATT ACC
S S D G S L E D D D Y H A T T E T I I T
361/121                               391/131
ATG COT ACA GAG TGT GAT TTT TTA ATG CAA GTG GAT GGA AAA CCC AAA TGT TGC TTC TTT
M P T E S D F L M Q V D G K P K C C F F
421/141                               451/151
AAA TTT AGC TGT AAA ATA CAA TAC AAT AAA GTG GTA AAG GGC CAA CTA TGG ATA TAT TTG
K F S S K I Q Y N K V V K A Q L W I Y L
481/161                               511/171
AGA CCC GTG GAG ACT COT ACA ACA GTG TTT GTG GAA ATC CTG ACA CTC ATC AAA COT ATG
R P V E T P T T V F V Q I L R L I K P M
541/181                               571/191
AAA GAC COT ACA AGG TAT ACT GGA ATC CGA TCT CTG AAA CTT GAC ATG AAC CCA GGC ACT
K D G T R Y T G I R S L K L D M N P G T
601/201                               631/211
GTT ATT TGG CAG AGC ATT GAT GTG AAG ACA GTG TTG CAA AAT TGG CTC AAA CAA COT GAA
G E W Q S I D V K T V L Q N W L K Q P E
661/221                               691/231
TCC AAC TTA GGC ATT GAA ATA AAA GGT TTA GAT GAG AAT GGT CAT GAT CTT GGT GTA ACC
S N L G I E I K A L D E N G H D L A V T
721/241                               751/251
TTG CCA CGA CCA GGA GAA GAT GGG CTG AAT CCC TTT TTA GAG GTC AAG GTA ACA GAC ACA
F P G P G E D G L N P F L E V K V T D T
781/261                               811/271
CCA AAA AGA TCC AGA AGG GAT TTT GGT CTT GAC TGT GAT GAG CAC TCA ACA GAA TCG CCA
P K R S R R D F G L D C D E H S T E S R
841/281                               871/291
TGC TGT COT TAC COT CTA ACT GTG GAT TTT GAA GCT CTT GGA TGG GAT TGG ATT ATC GCT
C C R Y P L T V D F E A L G W D W I I A
901/301                               931/311
CCT AAA AGA TAT AAG GGC AAT TAC TGC TCT GGA GAG TGT GAA TTT GTA TTT TTA CAA AAA
P K R Y K A N Y C S G E C E F V F L Q K
961/321                               991/331
TAT COT CAT ACT CAT CTG GTA CAC CAA CCA AAC CCC AGA GGT TCA GCA GGC COT TGC TGT
Y P H T H L V H Q A N P R G S A G P C C
1021/341                               1051/351
ACT CCC ACA AAG ATG TCT CCA ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA
T P T K M S P I N M L Y F N G K E Q I I
1081/361                               1111/371
TAT GGC AAA ATT CCA GGC ATG GTA GTA GAC CGC TGC GGC TGC TCA TCA
Y G K I P A M V V D R C G C S

```

FIGURE 14b

1/1
 ATG CAA AAA CTG CAA ATC TCT GTT TAT ATT TAC CTA TTT ATG CTG ATT GTT GGT GCC CCA
 M Q K L Q I S V Y I Y L F M L I V A G P
 61/21
 GTG GAT CTG AAT GAG AAC AGC GAG CAG AAG GAA AAT GTG GAA AAA GAG GGG CTG TGT AAT
 V D L N E N S E Q K E N V E K E G L C N
 121/41
 GCA TGT TTG TGG AGG GAA AAC ACT ACA TCC TCA AGA CTA GAA GCC ATA AAA ATC CAA ATC
 A C L W R E N T T S S R L E A I K I Q I
 181/61
 CTC AGT AAA CTT CGC CTG GAA ACA GCT CCT AAC ATC AGC AAA GAT GCT ATC AGA CAA CTT
 L S K L R L E T A P N I S K D A I R Q L
 241/81
 TTG CCC AAG GCT CCT CCA CTC CTG GAA CTG ATT GAT CAG TTC GAT CTC CAG AGA GAT GCC
 L P K A P P L L E L I D Q F D V Q R D A
 301/101
 AGC AGT GAC GGC TCC TTG GAA GAC GAT GAC TAC CAC GCC AGG ACG GAA ACG GTC ATT ACC
 S S D G S L E D D D Y H A R T E T V I T
 361/121
 ATG CCC ACG GAG TCT GAT CTT CTA ACG CAA GTG GAA GGA AAA CCC AAA TGT TGC TTC TTT
 M P T E S D L L T Q V E G K P K C C F F
 421/141
 AAA TTT AGC TCT AAG ATA CAA TAC AAT AAA CTA GTA AAG GCC CAA CTG TGG ATA TAT CTG
 K F S S K I Q Y N K L V K A Q L W I Y L
 481/161
 AGC CTT GTC AAG ACT CTT GCG ACA GTG TTT GTC CAA ATC CTG AGA CTC ATC AAA CCC ATC
 R P V H T P A T V F V Q I L R L I K P M
 541/181
 AAA GAC GGT ACA AGG TAT ACT GGA ATC CGA TCT CTG AAA CTT GAC ATG AAC CCA GGC ACT
 K D G T R Y T G I R S L K L D M N P G T
 601/201
 GGT ATT TGG CAG AGC ATT GAT GTG AAG ACA GTG TTG CAG AAC TGG CTC AAA CAA CTT GAA
 G I W Q S I D V K T V L Q N W L K Q P E
 661/221
 TCC AAC TTA GGC ATT GAA ATC AAA GGT TTA GAT GAG AAT GGC CAT GAT CTT GCT GTA ACC
 S N L G I E I K A L D E N G H D L A V T
 721/241
 TTC CCA GAA CCA GGA GAA GAT GGA CTG ACT CTT TTT TTA GAA GTC AAG GTA ACA GAC ACA
 F P E P G E D G L T P F L E V K V T D T
 781/261
 CCA AAA AGA TCT AGG AGA GAT TTT GGG CTT GAT TGT GAT GAA CAC TCC ACA GAA TCT CGA
 P K R S R R D F G L D C D E H S T E S R
 841/281
 TGC TGT CTT TAC CTT CTA ACT GTG GAT TTT GAA GCT TTT GGA TGG GAT TGG ATT ATT GCA
 C C R Y P L T V D F E A F G W D W I I A
 901/301
 CCT AAA AGA TAT AAG GCC AAT TAC TGC TCT GGA GAA TGT GAA TTT GTA TTT TTG CAA AAG
 P K R Y K A N Y C S G E C E F V F L Q K
 961/321
 TAT CTT CAT ACC CAT CTT GTG CAC CAA GCA AAC CCC AGA GGT TCA GCC GGC CCC TGC TGT
 Y P H T H L V H Q A N P R G S A G P C C
 1021/341
 ACT CTT ACA AAG ATC TCT CCA ATT AAT ATC CTA TAT TTT AAT GGC GAA GGA CAA ATA ATA
 T P T K H S P I N M L Y F N G E G Q I I
 1081/361
 TAC GCG AAG ATT CCA GCC ATG GTA GTA GAT CGC TGT GGG TGT TCA TGA
 Y G K I P A M V V D R C G C S *

FIGURE 14c

```

1/1                               31/11
ATC CAA AAG CTA GCA GTC TAT GTT TAT ATT TAC CTG TTC ATG CAG ATC GCG GTT CAT CCG
M Q K L A V Y V Y I Y L F M Q I A V D P
61/21                               91/31
CTG GCT CTG GAT GGC AGT AGT CAG CCC ACA GAG AAC GCT GAA AAA GAC GGA CTG TGC AAT
V A L E G S S Q P T E N A E K D G L C N
121/41                               151/51
GCT TGT ACC TGG AGA CAG AAT ACA AAA TCC TCC AGA ATA GAA GCC ATA AAA ATT CAA ATC
A C T W R Q N T K S S R I E A I K I Q I
181/61                               211/71
CTC AGC AAA CTG GCG CTG GAA CAA GCA CCT AAC ATT AGC AGG GAC GTT ATT AAG CAG CTT
L S K L R L E Q A P N I S R D V I K Q L
241/81                               271/91
TTA CCC AAA GCT CTT CCA CTG CAG GAA CTG ATT GAT CAG TAT GAT GTC CAG AGG GAC GAC
L P K A P P L Q E L I D Q Y D V Q R D D
301/101                               331/111
AGT AGC GAT GGC TGT TTG GAA GAC GAT GAC TAT CAT GCC ACA ACC GAG ACG ATT ATC ACA
S S D G S L E D D D Y H A T T E T I I T
361/121                               391/131
ATG CCT ACC GAG TGT GAT TTT CTT GTA CAA ATG GAG GGA AAA CCA AAA TGT TGC TTC TTT
M P T E S D F L V Q M E G K P K C C F F
421/141                               451/151
AAG TTT AGC TCT AAA ATA CAA TAT AAC AAA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTG
K F S S K I Q Y N K V V K A Q L W I Y L
481/161                               511/171
AGC CAA CTC CAA AAA CTT ACA AGC GTC TTT GTC CAG ATT CTG AGA CTC ATT AAG GCG ATG
R Q V Q K P T T V F V Q I L R L I K P M
541/181                               571/191
AAA GAC GGT ACA AGA TAT ACT GGA ATT CGA TCT TTG AAA CTT GAC ATG AAC CCA GGC ACT
K D G T R Y T G I R S L K L D M N P G T
601/201                               631/211
GCT ATC TGG CAG AGT ATT GAT GTG AAG ACA GTG CTG CAA AAT TGG CTC AAA CAG CTT GAA
G I W Q S I D V K T V L Q N W L K Q P E
661/221                               691/231
TCC AAT TTA GGC ATC CAA ATA AAA GCT TTT CAT GAG ACT GCA CCA GAT CTT GCT GTC ACA
S N L G I E I K A F D E T G R D L A V T
721/241                               751/251
TTC CCA GGA CCG GGT GAA GAT GGA TTG AAC CCA TTT TTA GAG GTC AGA GTT ACA GAC ACA
F P G P G E D G L N P F L E V R V T D T
781/261                               811/271
CCG AAA CCG TCC CCG AGA GAT TTT GCG CTT GAC TGT GAT GAG CAT TCA ACG GAA TCC CGA
P K R S R R D F G L D C D E H S T E S R
841/281                               871/291
TGT TGT CCG TAC CCG CTG ACA GTG GAT TTC GAA GCT TTT GGA TGG GAC TGG ATT ATA GCA
C C R Y P L T V D F E A F G W D W I I A
901/301                               931/311
CCT AAA AGA TAC AAA GCG AAT TAC TGC TCC GGA GAA TGC GAA TTT GTG TTT CTA CAG AAA
P K R Y K A N Y C S G E C E F V F L Q K
961/321                               991/331
TAC CCG CAC ACT CAC CTG GTA CAC CAA GCA AAT CCC AGA GCG TCA CCA GCG CTT TGC TGC
Y P H T H L V H Q A N P R G S A G P C C
1021/341                               1051/351
ACA CCC ACC AAG ATG TCC CCT ATA AAC ATG CTG TAT TTC AAT GGA AAA GAA CAA ATA ATA
T P T K M S P I N M L Y F N G K E Q I I
1081/361                               1111/371
TAT GGA AAG ATA CCA GCG ATG GTT GTA GAT CGT TGC GGG TGC TCA TGA
Y G K I P A M V V D R C G C S *

```

Chicken GDF-8

27/32

FIGURE 14d

1/1
 ATG ATT CAA AAA CCG CAA ATG TAT GTT TAT ATT TAC CTG TTT GTG CTG ATT GCT GCT GCG
 M I Q K P Q M Y V Y I Y L F V L I A A G
 61/21
 CCA GTC GAT CTA AAT GAG GAC AGT GAG AGA GAG GCG AAT GTG GAA AAA GAG GCG CTG TGT
 P V D L N E D S E R E A N V E K E G L C
 121/41
 AAT GCG TGT GCG TGG AGA CAA AAC ACA AGC TAC TCC AGA ATA GAA GCG ATA AAA ATT CAA
 N A C A W R Q N T R Y S R I E A I K I Q
 191/61
 ATC CTC AGT AAA CTC CCG CTG GAA ACA GCG CCT AAC ATC AGC AAA GAT GCT ATA AGA CAA
 I L S K L R L E T A P N I S K D A I R Q
 241/81
 CTT CTC CCG AGA GCG CCT CCA CTC CCG GAA CTC ATC GAT CAG TAC GAC CTC CAG AGC GAT
 L L P R A P P L R E L I D Q Y D V Q R D
 301/101
 GAC AGC AGT GAC GCG TGT TTG GAA GAT GAC GAT TAT CAC GCT ACC ACG GAA ACA ATC ATT
 D S S D G S L E D D D Y H A T T E T I I
 361/121
 ACC ATG CTT ACC GAG TGT GAC TTT CTA ATG CAA GCG GAT GSA AAG CCC AAA TGT TGC TTT
 T M P T E S D F L M Q A D G K P K C C F
 421/141
 TTT AAA TTT ACC TGT AAA ATA CAG TAC AAC AAA GTG GTA AAG GCG CAG CTG TGG ATA TAT
 F K P S S K I Q Y N K V V K A Q L W I Y
 481/161
 CTG AGA GCG GTC AAG ACT CTT ACA ACA GTG TTT GTG CAA ATC CTG AGA CTC ATC AAA CCG
 L R A V E T P T T V F V Q I L R L I K F
 541/181
 ATG AAA GAC GGT ACA AGC TAT ACC GGA ATC CCA TGT CTG AAA CTT GAC ATG ACC CCA GCG
 M K D G T R Y T G I R S L K L D M S P G
 601/201
 ACT GGT ATT TGG CAG AGT ATT GAT GTG AAG ACA GTG TTG CAA AAT TGG CTC AAA CAG CCT
 T G I W Q S I D V K T V L Q N W L K Q P
 661/221
 GAA TCG AAG TTA GCG ATT GAA ATC AAA GCT TTG GAT GAG AAT GCG CAT GAT CTT GCT GTA
 E S N L G I E I K A L D E N G H D L A V
 721/241
 ACC TTC CCA GGA CCA GGA GAA GAT GCG CTG AAT CCG TTT TTA GAA CTC AAA GTA ACA GAC
 T F P G P G E D G L N P F L E V K V T D
 781/261
 ACA CCG AAG AGG TCG CCG AGA GAC TTT GGG CTT GAC TGT GAT GAA CAC TCG ACG GAA TCG
 T P K R S R R D F G L D C D E H S T E S
 841/281
 CCG TCG TGT CCG TAC CCG CTC ACG GTC GAT TTC GAA GCG TTT GGA TGG GAC TGG ATT ATT
 R C C R Y P L T V D F E A F G W D W I I
 901/301
 GCA CCG AAA AGA TAT AAG GGT AAT TAC TCG TCT GCA CAG TGT GAA TTT GTG TTC TTA CAA
 A P K R Y K A N Y C S G E C E F V F L Q
 961/321
 AAA TAT CCG CAT ACT CAT CTT GTG CAC CAA GCA AAC CCG AGA GCG TCG GCA GCG CTT TCG
 X Y P H T H L V H Q A N P R G S A G P C
 1021/341
 TCG ACG CCA ACA AAA ATG TGT CCG ATT AAT ATG CTA TAT TTT AAT GCG AAA GAA CAA ATA
 C T P T K M S P I N M L Y F N G K E Q I
 1081/361
 ATA TAT GCG AAA ATT CCA GCG ATG GTA GTA CAC CCG TGT CCG TCG TCG TGA
 I Y G K I P A M V V D R C G C S

28/32

FIGURE 14e

1/1
 ATG CAA AAG CTA GCA GTC TAT GTT TAT ATT TAC CTG TTC ATG CAG ATT TTA GTT CAT CCG
 H Q K L A V Y V Y I Y L F M Q I L V H P
 61/21
 CTG GGT CTT GAT GGC AGT AGT CAG CCC ACA GAG AAC GGT GAA AAA GAC GGA CTG TGC AAT
 V A L D G S S Q P T E N A E K D G L C N
 121/41
 GGT TGC ACC TGG AGA CAG AAT ACT AAA TGC TCC ACA ATA GAA CCC ATA AAA ATT CAA ATC
 A C T W R C N T K S S R I E A I K I Q I
 181/61
 CTC AGC AAA CTG GGC CTG GAA CAA GCA CCT AAC ATT AGC AGC GAC GTT ATT AAA CAA CTT
 L S K L R L E Q A P N I S R D V I K Q L
 241/81
 TTA CCC AAA GGT CTT CCG CTG CAG CAA CTG ATT GAT CAG TAT CAC CTC CAG AGA GAC GAC
 L P K A P P L Q E L I D Q Y D V G R D D
 301/101
 AGT AGC GAT GGC TGT TTT GAA GAC GAT GAC TAT CAT GGC ACA ACC GAA ACC ATT ATC ACA
 S S D G S L E D D D Y K A T T E T I I T
 361/121
 ATG CCT ACC GAG TGT GAT TTT CTT GTA CAA ATG CAG CGA AAA CCA AAA TGT TGC TTC TTT
 M P T E S D F L V Q M E G K P K C C F F
 421/141
 AAG TTT ACC TGT AAA ATA CAA TAT AAC AAA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTC
 K F S S K I Q Y N X V V K A Q L W I Y L
 481/161
 AGG CAA GTC GAA AAA CTT ACA ACC CTG TTT CTC CAG ATC CTC ACA CTC ATT AAA CCC ATC
 R C V Q N P T T V F V Q I L R L I K P M
 541/181
 AAA CAC GGT ACA AGA TAT ACT GGA ATT GGA TGT TTT AAA CTT GAC ATG AAC CCA GGC ACT
 K D G T R Y T G I R S L K L D M N P G T
 601/201
 GGT ATC TGG CAG AGT ATT GAT GTC AAC ACA GTG TTT CAA AAT TGG CTC AAA CAG CTT GAA
 C I W Q S I D V K T V L Q N W L R Q P E
 661/221
 TGC AAT TTA GGC ATC GAA ACA AAA GGT TTT GAT GAG AAT GGA CGA GAT CTT CTT GTA ACA
 S N L G I E I K A F D E N G R D L A V T
 721/241
 TTC GCA GCA CCA GGT GAA GAT GGA CTC AAC CCA TTT TTA CAG CTC AGA GTT ACA GAC ACA
 F P G P G E D C L N E F L E V R V T D T
 781/261
 GGA AAA CCG TGC CCG ACA GAT TTT GGC CTT GAT TGC GAC GAG CAC TCA ACC GAA TGT CCA
 F K R S E A D F C L D C D E H S T E S R
 841/281
 TGT TGT CCG TAC CCG CTC ACA GTG GAT TTT GAA GGT TTT GGA TGG CAC TGG ATT ATA GCA
 C C R Y P L T V D F E A P G W D W I I A
 901/301
 CCT AAA ACA TAC AAA GGT AAT TAC TGC TGT GGA GAA TGT GAA TTC GTA TTT CTA CAG AAA
 P K R Y Z A N Y C S G E C E F V F L G K
 961/321
 TAC CCG CAC ACT CAC CTC GTA CAC CAA GCA AAT CCA AGA GGC TCA CCA GGC CTT TGC TGC
 Y P H T H L V H Q A N P R C S A G P C C
 1021/341
 ACA CCC ACC AAG ATG TCC CTT ATA AAC ATC CTC TAT TTC AAT GGA AAA CAA CAA ATA ATA
 T P T K M S P I N M L Y F N G K E G I I
 1081/361
 TAT GGA AAG ATA CCA GGC ATG GTT GTA CAT CTT TGC CCG TCC TCA TCA
 Y G K I P A M V V D R C C C S

29/32

1/1

ATG CAA AAA CTG CAA ATC TAT TAT ATT TAC CTG TTT ATG CTG ATT GTT GCT GGA CCC
M Q K L Q I Y V Y I Y L F M L I V A G P

61/21

GTG GAT CTG AAT GAG AAC AGC GAG CAA AAG GAA AAT GTG GAA AAA GAG GGG CTG TGT AAT
V D L N E N S E Q K E N V E K E G L C N

121/41

GCA TGT ATG TGG ACA CAA AAC ACT AAA TCT TCA AGA CTA GAA GCC ATA AAA ATT CAA ATC
A C M W R Q N T K S S R L E A I K I Q I

181/61

CTC AGT AAA CTT CGC CTG GAA ACA GCT CCT AAC ATT AGC AAA GAT GCT ATA AGA CAA CTT
L S K L R L E T A P N I S K D A I R Q L

241/91

TTG CCC AAA GGT COT CCA CTC CGG GAA CTG ATT GAT CAG TAC GAT GTC CAG AGA GAT GAC
L P K A P P L R E L I D Q Y D V Q R D D

301/101

AGC AGT GAT GGC TCC TTG GAA GAT GAT GAT TAT CAC GGT ACG ACG GAA ACG ATC ATT ACC
S S D G S L E D D B Y H A T T E T I I T

361/121

ATG CCT ACA GAG TGT GAT CTT CTA ATG CAA GTG GAA GGA AAA CCC AAA TGC TGC TTC TTT
M P T E S D L L M Q V E G K P K C C F F

421/141

AAA TTT AGC TCT AAA ATA CAA TAC AAT AAA GTA GTA AAG GCC CAA CTG TGG ATA TAT CTG
K F S S K I Q Y N K V V K A Q L W I Y L

481/161

AGA CCC GTC AAG ACT COT ACA ACA GTG TTT GTG CAA ATC CTG AGA CTC ATC AAA CCC ATG
R P V K T P T T V F V Q I L R L I K P M

541/181

AAA GAC GGT ACA AGG TAT ACT GGA ATC CGA TCT CTG AAA CTT GAC ATG AAC CCA GGC ACT
K D G T R Y T G I R S L K L D M N P G T

601/201

GGT ATT TGG CAG AGC ATT GAT GTG AAG ACA GTG TTG CAA AAT TGG CTC AAA CAA COT GAA
G I W Q S I D V K T V L Q N W L K Q P E

661/221

TCC AAC TTA GGC ATT GAA ATC AAA GCT TTA GAT GAG AAT GGT CAT GAT CTT GCT GTA ACC
S N L G I E I K A L D E N G H D L A V T

721/241

CTC CCA GGA CCA GGA GAA GAT GGG CTG AAT CCC TTT TTA GAA GTC AAG GTA ACA GAC ACA
F P G P G E D G L N P F L E V K V T D T

781/261

CCA AAA AAT TCC AGG AGA GAT TTT GGA CTC GAC TGT GAT GAG CAC TCA ACA GAA TCT CGA
F K R S R R D F G L D C D E H S T E S R

841/281

TCC TGT COT TAC COT CTA ACT GTG GAT TTT GAA GCT TTT GGA TGG GAC TGG ATT ATT GCA
C C R Y P L T V D F E A F G W D W I I A

901/301

CCC AAA AGA TAT AAG GCC AAT TAC TCC TCT GGA GAG TGT GAA TTT GTA TTT TTA CAA AAA
P K R Y K A N Y C S G E C E F V F L Q K

961/321

TAC COT CAC ACT CAT CTT GTG CAC CAA GCA AAC CCC AGA GGT TCA GCA GGC CCC TGC TGT
Y F E T E L V H Q A N P R G S A G P C C

1021/341

ACT CCC ACA AAG ATG TCT CCA ATC AAT ATG CTA TAT TTT AAT CGC AAA GAA CAA ATA ATA
T P T K M S P I N M L Y F N G K E Q I I

1081/361

TAT GGG AAA ATT CCA GCC ATG GTA GTA GAT CGC TGT GGG TGC TCA TGA
Y G K I P A M V V D R C G C S *

Porcine GDF-8

FIGURE 14F

30/32

1/1
 ATG CAA AAA CTG CAA ATC TTT GTT TAT ATT TAC CTA TTT ATG CTG CTT GTT GCT GGC CCA
 M Q K L C I F V Y I Y L F M L L V A G P
 61/21
 GTG GAT CTG AAT GAG AAC AGC GAG CAG AAG GAA AAT GTG GAA AAA AAG GGG CTG TGT AAT
 V D L N E N S E Q K E N V E K K G L C N
 121/41
 GCA TGC TGG TGG AGA CAA AAC AAT AAA TCC TCA AGA CTA GAA GCC ATA AAA ATC CAA ATC
 A C L W R Q N N K S S R L E A I K I Q I
 191/61
 CTC AGT AAG CTT CCG CTG GAA ACA GGT CCT AAC ATC AGC AAA GAT GCT ATA AGA CAA CTT
 L S K L R L E T A P N I S K D A I R Q L
 241/91
 TGG CCC AAG GGT CTT CCA CTG CGG GAA CTG ATT GAT CAG TAC GAT GTC CAG AGA GAT GAC
 L P K A P P L R E L I D Q Y D V Q R D D
 301/101
 AGC AGC GAC GGC TCC TGG GAA GAC GAT GAC TAC CAC GTT ACG ACG GAA ACG GTC ATT ACC
 S S D G S L E D D D Y H V T T E T V I T
 361/121
 ATG CCC ACG GAG TGT GAT CTT CTA GCA GAA GTG CAA GAA AAA CCC AAA TGT TGC TTC TTT
 M P T E S D L L A E V Q E K P K C C F F
 421/141
 AAA TTT AGC TGT AAG ATA CAA CAC AAT AAA GTA GTA AAG GCC CAA CTG TGG ATA TAT CTG
 K F S S K I Q H N K V V K A Q L W I Y L
 481/161
 AGA CCT GTC AAG ACT CCT ACA ACA GTG TTT GTG CAA ATC CTG AGA CTC ATC AAA CCC ATG
 R P V K T P T T V F V Q I L R L I X P M
 541/181
 AAA GAC GGT ACA AGC TAT ACT GGA ATC CGA TGT CTG AAA CTT GAC ATG AAC CCA GGC ACT
 K D G T R Y T G I R S L K L D M N P G T
 601/201
 GGT ATT TGG CAG AGC ATT GAT GTG AAG ACA GTG TGG CAA AAC TGG CTC AAA CAA CCT GAA
 G I W Q S I D V K T V L Q N W L K Q P E
 661/221
 TCC AAC TTA GGC ATT GAA ATC AAA GCT TTA GAT GAG AAT GGT CAT GAT CTT GCT GTA ACC
 S N L G I E I K A L D E N G H D L A V T
 721/241
 TTC CCA GAA CCA GGA GAA GAA GGA CTG AAT CCT TTT TTA GAA GTC AAG GTA ACA GAC ACA
 F P E P G E E G L N P F L E V K V T D T
 781/261
 CCA AAA AGA TCT AGG AGA GAT TTT GGG CTT GAT TGT GAT GAG CAC TCC ACA GAA TCT CGA
 P K R S R R D F G L D C D E H S T E S R
 841/281
 TGC TGT CGT TAC CCT CTA ACT GTG GAT TTT GAA GCT TTT GGA TGG GAT TGG ATT ATT GCA
 C C R Y P L T V D F E A F C W D W I I A
 901/301
 CCT AAA AGA TAT AAG GCC AAT TAC TGC TCT GGA GAA TGT GAA TTT TTA TTT TTG CAA AAG
 P K R Y K A N Y C S G E C E F L F L Q K
 961/321
 TAT CCT CAT ACC CAT CTT GTG CAC CAA GCA AAC CCC AAA GGT TCA GCC GGC CCT TGC TGT
 Y P H T H L V H Q A N P K G S A G P C C
 1021/341
 ACT CCT ACA AAG ATG TGT CCA ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA
 T P T K M S P I N M L Y F N G K E Q I I
 1081/361
 TAT GGG AAG ATT CCA GGC ATG GTA GTA GAT CGC TGT GGC TGC TCA TGA
 Y G K I P G M V V D R C G C S

Ovine GDF-8

FIGURE 14g

N	M	Q	K	L	Q	M	Y	V	Y	I	Y	L	F	M	L	I	A	A	G	P	V	D	L	N	E	G	S	E	R	E	A	N	V	E	K	E	G	L	C	murine	
M	-	Q	K	P	Q	M	Y	V	Y	I	Y	L	F	M	L	I	A	A	G	P	V	D	L	N	E	D	S	E	R	E	A	N	V	E	K	E	G	L	C	rat	
M	-	Q	K	L	Q	L	C	V	Y	I	Y	L	F	M	L	I	V	A	G	P	V	D	L	N	E	N	S	E	Q	K	E	N	V	E	K	E	G	L	C	human	
M	-	Q	K	L	Q	I	C	V	Y	I	Y	L	F	M	L	I	V	A	G	P	V	D	L	N	E	N	S	E	Q	K	E	N	V	E	K	E	G	L	C	baboon	
M	-	Q	K	L	Q	I	F	V	Y	I	Y	L	F	M	L	L	V	A	G	P	V	D	L	N	E	N	S	E	Q	K	E	N	V	E	K	E	K	G	L	C	porcine
M	-	Q	K	L	Q	I	S	V	Y	I	Y	L	F	M	L	L	V	A	G	P	V	D	L	N	E	N	S	E	Q	K	E	N	V	E	K	E	G	L	C	ovine	
M	-	Q	K	L	A	V	Y	V	Y	I	Y	L	F	M	Q	I	A	V	D	P	V	A	L	D	G	S	S	Q	P	T	E	N	A	E	K	D	G	L	C	bovine	
M	-	O	K	L	A	V	Y	V	Y	I	Y	L	F	M	Q	I	L	V	H	P	V	A	L	D	G	S	S	Q	P	T	E	N	A	E	K	D	G	L	C	chicken	
M	-	O	K	L	A	V	Y	V	Y	I	Y	L	F	M	Q	I	L	V	H	P	V	A	L	D	G	S	S	Q	P	T	E	N	A	E	K	D	G	L	C	turkey	
N	A	C	A	W	R	Q	N	T	R	Y	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	murine	
N	A	C	A	W	R	Q	N	T	R	Y	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	rat	
N	A	C	T	W	R	Q	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	V	I	R	Q	human	
N	A	C	T	W	R	Q	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	baboon	
N	A	C	M	W	R	Q	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	porcine	
N	A	C	L	W	R	Q	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	ovine	
N	A	C	L	W	R	E	N	T	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	T	A	P	N	I	S	K	D	A	I	R	Q	bovine		
N	A	C	T	W	R	Q	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	Q	A	P	N	I	S	R	D	V	I	K	O	chicken	
N	A	C	T	W	R	O	N	T	K	S	S	R	I	E	A	I	K	I	Q	I	L	S	K	L	R	L	E	Q	A	P	N	I	S	R	D	V	I	K	O	turkey	
L	L	P	R	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	murine	
L	L	P	R	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	rat	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	human	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	baboon	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	porcine	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	V	I	ovine	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	V	I	bovine	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	chicken	
L	L	P	K	A	P	P	L	R	E	L	I	D	Q	Y	D	V	Q	R	D	D	S	S	D	G	S	L	E	D	D	D	Y	H	A	T	T	E	T	I	I	turkey	
T	M	P	T	E	S	D	F	L	M	Q	A	D	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	V	V	K	A	Q	L	W	I	Y	murine	
T	M	P	T	E	S	D	F	L	M	Q	A	D	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	V	V	K	A	Q	L	W	I	Y	rat	
T	M	P	T	E	S	D	F	L	M	Q	V	D	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	V	V	K	A	Q	L	W	I	Y	human	
T	M	P	T	E	S	D	L	L	M	O	V	E	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	V	V	K	A	Q	L	W	I	Y	baboon	
T	M	P	T	E	S	D	L	L	A	E	V	Q	E	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	H	N	K	V	V	K	A	Q	L	W	I	Y	porcine	
T	M	P	T	E	S	D	L	L	T	Q	V	E	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	L	V	K	A	Q	L	W	I	Y	ovine	
T	M	P	T	E	S	D	F	L	V	Q	M	E	G	K	P	K	C	C	F	F	K	F	S	S	K	I	Q	Y	N	K	V	V	K	A	Q	L	W	I	Y	bovine	
T	M	P	T	E	S	D	F	L	V	Q	M	E	G	K	P	K	C	C	F	F	K	F	S	S	K	I	O	Y	N	K	V	V	K	A	Q	L	W	I	Y	chicken	
T	M	P	T	E	S	D	F	L	V	Q	M	E	G	K	P	K	C	C	F	F	K	F	S	S	K	I	O	Y	N	K	V	V	K	A	Q	L	W	I	Y	turkey	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	S	P	G	murine	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	rat	
L	R	P	V	E	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	human	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	baboon	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	porcine	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	ovine	
L	R	P	V	K	T	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	bovine	
L	R	Q	V	Q	K	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	chicken	
L	R	Q	V	Q	K	P	T	T	V	F	V	Q	I	L	R	L	I	K	P	H	K	D	G	T	R	Y	T	G	I	R	S	L	K	L	D	M	N	P	G	turkey	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	murine	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	rat	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	human	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	baboon	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	porcine	
T	G	I	W	Q	S	I	D	V	K	T	V	L	Q	N	W	L	K	Q	P	E	S	N	L	G	I	E	I	K	A	L	D	E	N	G	H	D	L	A	V	ovine	
T	G	I																																							

FIGURE 15a

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T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		murine
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		rat
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		human
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		baboon
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		porcine
T	F	P	E	P	G	E	E	G	L	N	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		ovine
T	F	P	S	P	G	E	D	G	L	T	P	F	L	E	V	K	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		bovine
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	R	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		chicken
T	F	P	G	P	G	E	D	G	L	N	P	F	L	E	V	R	V	T	D	T	P	K	R	S	R	R	D	F	G	L	D	C	D	E	H	S	T	E	S		turkey

R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		murine
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		rat
R	C	C	R	Y	P	L	T	V	D	F	E	A	E	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		human
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		baboon
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	L	F	L	Q		porcine
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		ovine
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		bovine
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		chicken
R	C	C	R	Y	P	L	T	V	D	F	E	A	F	G	W	D	W	I	I	A	P	K	R	Y	K	A	N	Y	C	S	G	E	C	E	F	V	F	L	Q		turkey

K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		murine
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		rat
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		human
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		baboon
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		porcine
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	E	G	Q	I		ovine
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		bovine
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		chicken
K	Y	P	H	T	H	L	V	H	Q	A	N	P	R	G	S	A	G	P	C	C	T	P	T	K	M	S	P	I	N	M	L	Y	F	N	G	K	E	Q	I		turkey

I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																								murine
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																							rat	
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																							human	
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																								baboon
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																								porcine
I	Y	G	K	I	P	G	M	V	V	D	R	C	G	C	S																								ovine
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																							bovine	
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																							chicken	
I	Y	G	K	I	P	A	M	V	V	D	R	C	G	C	S																							turkey	

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIGURE 15b

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/02479

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 5/00, 15/00, 15/09, 15/63

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 800/2; 435/172.3, 69.1, 320.1, 325; 530/350, 387.1; 514/2, 44; 424/9.21

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MCDOWELL et al. Effects of Exogenous Growth Hormone on Milk Production and Nutrient Uptake by Muscle and Mammary Tissues of Dairy Cows in Mid-Lactation. Australian Journal of Biological Sciences, Vol. 40, No. 3, pages 295-306, see Abstract.	13
Y	EVOCK et al. Pituitary Porcine Growth Hormone (pGH) and a Recombinant pGH Analog Stimulate Pig Growth Performance in a Similar Manner. Journal of Animal Science, Vol. 66, No. 8, pages 1928-1941, see Abstract.	14

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 25 MARCH 1998	Date of mailing of the international search report 15 JUN 1998 <i>[Signature]</i> JILL D. SCHMUCK
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/02479

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	FLAKOLL et al. Influence of Alpha-Ketoisocaproate on Lamb Growth, Feed, Conversion, and Carcass Composition. Journal of Animal Science, Vol. 69, No. 4, pages 1461-1467, see Abstract.	15
Y	DELI et al. Biochemical Study of Muscle Samples from Chicken Embryos Affected by Wofatox 50 EC. Archives of Toxicology, Vol. 8, pages 277-279, see Abstract.	16
Y	FAULKNER et al. Effect of Testosterone Propionate on Performance and Carcass Characteristics of Heifers and Cows. Journal of Animal Science, Vol. 67, No. 8, pages 1907-1915, see Abstract.	12
Y	ZHU et al. Survey of Major Histocompatibility Complex Class II Haplotypes in Four Turkey Lines Using Restriction Fragment Length Polymorphism Analysis with Nonradioactive DNA Detection. Poultry Science, Vol. 74, No. 7, pages 1067-1073, see Abstract.	11

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/02479

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

800/2; 435/172.3, 69.1, 320.1, 325; 530/350, 387.1; 514/2, 44; 424/9.21

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, BIOSIS, EMBASE, CAPLUS, WPIDS, CONFSCI

search terms: growth differentiation factor-8, GDF-8, transgene, increased muscle, reduced cholesterol, mouse, pigs or porcine, cows or bovine, sheep or ovine, piscine, chicken or turkey or avian